

Query Match 80.5%; Score 681; DB 1; Length 192;
Best Local Similarity 79.4%; Pred. No. 1e-57;
Matches 131; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 27 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 86
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 87 IEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 146
QY 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165
DB 147 PPDTTPAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 191

RESULT 8

JC7699
erythropoietin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C:Accession: JC7699
R:Wen, D.; Boissel, J.
Biochem. Biophys. Res. Commun. 284, 823-827, 2001
A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
A:Reference number: JC7699; MUID:21290682; PMID:11396976
A:Contents: Kidney
A:Accession: JC7699
A:Molecule type: DNA
A:Residues: 1-195 <VIL>
A:CROSS-references: GB:AF290943
C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
cytes.
C:Genetics:
A:Gene: epo
C:Superfamily: erythropoietin
C:Keywords: glycoprotein; kidney

Query Match 80.4%; Score 680.5; DB 2; Length 195;
Best Local Similarity 81.3%; Pred. No. 1.2e-57;
Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 29 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 88
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 89 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 148

QY 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165
DB 149 PPEAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 194

RESULT 9

146578
erythropoietin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146578
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: 146083; MUID:93372347; PMID:8364201
A:Accession: 146578
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <WEN>
A:CROSS-references: UNIPROT:P49157; GB:L10607; NID:G164445; PID:AAA31029.1; PID:G164446
C:Superfamily: erythropoietin

Query Match 80.1%; Score 678; DB 2; Length 190;
Best Local Similarity 82.0%; Pred. No. 2e-57;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 23 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 82
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 83 MEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 142
QY 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165
DB 143 LPDASPSSATPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 189

RESULT 10

146199
erythropoietin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146199
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: 146083; MUID:93372347; PMID:8364201
A:Accession: 146199
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <WEN>
A:CROSS-references: UNIPROT:P33707; GB:L13027; NID:G290087; PIDN:AAA30842.1; PID:G552347
C:Superfamily: erythropoietin

Query Match 75.4%; Score 638; DB 2; Length 175;
Best Local Similarity 81.0%; Pred. No. 1.2e-53;
Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 23 APPRLICDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 82
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 83 LEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 142
QY 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 153
DB 143 LPDASPSSATPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 175

RESULT 11

G02729
thrombopoietin - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02729
R:Im, S.
Submitted to the EMBL Data Library, May 1996
A:Reference number: H01637
A:Accession: G02729
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <IMX>
A:CROSS-references: EMBL:U59493; NID:G1401245; PIDN:AA03392.1; PID:G1401246
C:Genetics:
A:Gene: hTPO

Query Match 10.6%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.71;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 120
 DB 83 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 142
 QY 121 PPDAASAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 165
 DB 143 LPEATSAAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 187

RESULT 5 /
 S28148
 erythropoietin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: S28148; EMBL:152743
 R:Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
 Biochim. Biophys. Acta 1171, 99-102, 1992
 A:Title: Nucleotide sequence of rat erythropoietin.
 A:Reference number: S28148; MUID:93042015; PMID:1420369
 A:Accession: S28148
 A:Molecule type: mRNA
 A:Residues: 1-192 <NAG>
 A:Cross-references: UNIPROT:P29676; GB:D10763; NID:G220735; PIDN:BAA01593.1; PID:G220736
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology.
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I62743
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 4-192 <RES>
 A:Cross-references: GB:L10608; NID:G204060; PIDN:AAA41126.1; PID:G204061
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.9%; Score 701; DB 1; Length 192;
 Best Local Similarity 82.4%; Pred. No. 1.3e-59;
 Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLEAKEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVQQA 60
 DB 27 APPRLICDSRVLELYLEAKEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVQQA 86
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 120
 DB 87 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 146
 QY 121 PPDAASAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 165
 DB 147 PPDAASAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 191

RESULT 6
 I46401
 erythropoietin precursor - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: I46401; I47077
 R:Fu, P.; Evans, B.; Lim, G. B.; Moritz, K.; Wintour, E. M.
 Mol. Cell. Endocrinol. 93, 107-116, 1993
 A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pi
 A:Reference number: I46401; MUID:93351736; PMID:8349021
 A:Accession: I46401
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-194 <FX>
 A:Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:G3395049; PIDN:CAA80848.1; PID:G339501
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology.
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I47077
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 4-15, 'L', 17-107, 'P', 109-194 <WEN>
 A:Cross-references: GB:L10610; NID:G165876; PIDN:AAA31518.1; PID:G165877
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-194/Product: erythropoietin #status predicted <MAT>
 F:34-189,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 81.0%; Score 685.5; DB 1; Length 194;
 Best Local Similarity 81.9%; Pred. No. 3.9e-58;
 Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLELYLEAKEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVQQA 60
 DB 28 APPRLICDSRVLELYLEAKEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVQQA 87
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 120
 DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGRLSLTTLRALGAQKEAIS 147
 QY 121 PPDAASAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 165
 DB 148 LPDATPSAAPLRITADTFKFLFRVYSNFRGKLYTGACRTGD 193

RESULT 7
 A24902
 erythropoietin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
 C:Accession: A24902; A24901
 R:Shoenmaker, C. B.; Mitsock, L. D.
 Mol. Cell. Biol. 6, 849-858, 1986
 A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
 A:Reference number: A24902; MUID:87039105; PMID:3773894
 A:Accession: A24902
 A:Molecule type: DNA
 A:Residues: 1-192 <SHO>
 A:Cross-references: UNIPROT:P07321
 A:Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 as
 R:McDonald, J. D.; Lin, F. K.; Goldwasser, E.
 Mol. Cell. Biol. 6, 842-848, 1986
 A:Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene.
 A:Reference number: A24901; MUID:87039104; PMID:3022133
 A:Accession: A24901
 A:Molecule type: DNA
 A:Residues: 1-67, 'P', 69-192 <MCD>
 A:Cross-references: GB:M12930; NID:G193086; PIDN:AAA37570.1; PID:G387152
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C:Genetics:
 A:Introns: 5/1; 52/3; 81/3; 141/3
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

QY	121	PPDASAAPIRLTIITADTFKLFVYSNFIKGLKLYTGEACRTGD	165
Db	147	LPDASAAPIRLTIITADTFKLFVYSNFIKGLKLYTGEACRRGD	191
RESULT 5			
Q867B1		PRELIMINARY;	PRT; 192 AA.
ID	Q867B1;		
AC	01-JUN-2003 (TREMELrel. 24, Created)		
DT	01-JUN-2003 (TREMELrel. 24, Last sequence update)		
DT	01-MAR-2004 (TREMELrel. 26, Last annotation update)		
DE	Erythropoietin.		
GN	Name=EPO;		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
NCBI_TaxID=9796;	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RC	PubMed=14719696;		
RA	Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,		
RA	Kijima-Suda I.;		
RT	"Nucleotide sequence of equine erythropoietin and characterization of		
RL	region-specific antibodies,"		
RL	Am. J. Vet. Res. 65:15-19(2004).		
DR	EMBL; AB100030; BAC55239.1; -.		
DR	HSP; F01588; IBUY.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005128; F:erythropoietin receptor binding; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR009079; 4 helix cytokine.		
DR	InterPro; IPR001323; EPO_TPO_		
DR	InterPro; IPR003013; Erythroptn.		
DR	Pfam; PF00758; EPO_TPO; 1.		
DR	FIRSF; FIRSF001951; EPO; 1.		
DR	PRINTS; PS00272; ERYTHROPTN.		
DR	PROSITE; PS00817; EPO_TPO; 1.		
SQ	SEQUENCE 192 AA; 20984 MW; E02D09849B09C4F CRC64;		
Query Match	85.5%;	Score 723;	DB 2; Length 192;
Best Local Similarity	84.8%;	Pred. No. 1.2e-60;	
Matches 140;	Conservative 10;	Mismatches 15;	Indels 0; Gaps 0;
QY	1	APPLICDSRVLERYLLEAKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVQQA	60
Db	27	APPLICDSRVLERYLLEAREENITMGCAGCSFGENVTPDTKYNFYAKRMEVQQA	86
QY	61	VEVWQGLALLSEAVLRQALLVNSOPWEPLQHVVDKAVGSLRTTLRAIQAQKEALS	120
Db	87	VEVWQGLALLSEALQQALLANSQPSETLRUHVVDKAVSSRLSTSLRAIQAQKEALS	146
QY	121	PPDASAAPIRLTIITADTFKLFVYSNFIKGLKLYTGEACRTGD	165
Db	147	PPDASAAPIRLTFADVTDLCKLFRIYSNFIKGLKLYTGEACRRGD	191
RESULT 6			
EPO_FELCA		STANDARD;	PRT; 192 AA.
ID	EPO_FELCA		
AC	P33708;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Erythropoietin precursor.		
GN	Name=EPO;		
OS	Felis silvestris catus (Cat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
NCBI_TaxID=9685;	[1]		
RP	SEQUENCE FROM N.A.		

QY 1 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 60
DB 28 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 147
QY 121 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 148 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 192

RESULT 2
AAE22357 PRELIMINARY; PRT; 193 AA.
AC AAP22357; (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein EPO.
GN EPO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Wilson R.;
RT "Toward a complete human genome sequence."
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Deebbar A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
RT "The sequence of Homo sapiens BAC clone RP11-335D7."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009488; AAP22357.1; -.
KW Hypothetical protein.
SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
Query Match 100.0%; Score 846; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.4e-72;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 60
DB 28 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 147
QY 121 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 148 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 192

RESULT 3
EPO_MACFA

ID EPO_MACFA STANDARD; PRT; 192 AA.
AC P07865;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8705236; PubMed=2877922;
RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
Fox G.M., Chen K.K., Castro M., Suggs S.;
RT "Monkey erythropoietin gene: cloning, expression and comparison with
the human erythropoietin gene."
RL Gene 44:201-209(1986).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; M18189; AAA36841.1; -.
DR PIR; JQ0173; JQ0173.
DR HSSP; P01588; 1CN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropoietin.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR0272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1..27.
FT CHAIN 28..192.
FT DISULFID 34..187.
FT DISULFID 56..60.
FT CARBOHYD 51..51.
FT CARBOHYD 65..65.
FT CARBOHYD 110..110.
FT CARBOHYD 152..152.
SQ SEQUENCE 192 AA; 21113 MW; E8A900F442AD4522 CRC64;
Query Match 90.4%; Score 764.5; DB 1; Length 192;
Best Local Similarity 91.5%; Pred. No. 1.4e-64;
Matches 151; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 60
DB 28 APPRLICDSRVLYRLLVLEAKAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLRSITLLRALGAQKEAIS 146
QY 121 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
DB 147 PPDAASAAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 191

Db 147 PDATQAPLRTTADTFCKLFRVYNSFLRGKLYTGACRGD 191

RESULT 8

Q6PWUS PRELIMINARY; PRT; 206 AA.
 AC Q6PWUS
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Erythropoietin
 OS Canis familiaris (Dog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney
 RA Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.,
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY572971; AAS77874.1; -
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 SQ SEQUENCE 206 AA; 22666 MW; 1BEC64A02CE4F5B0 CRC64;
 Query Match 81.9%; Score 693; DB 2; Length 206;
 Best Local Similarity 81.2%; Pred. No. 9.6e-58;
 Matches 134; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCSLNENITVPTKVNFKYAKMEVGQQA 60
 Db 41 APPRLICDSRVLELYLEAKAEENITTCGAHCSLNENITVPTKVNFKYAKMEVGQQA 100
 QY 61 VEWGGLALSSAVLRGQALLVNSQWEPLOLHVYDKAVSLRSLTLLRALGAKREMS 120
 Db 101 LEVWGGLALSSAVLRGQALLVNSQWEPLOLHVYDKAVSLRSLTLLRALGAKREMS 160
 QY 121 PDAAASAPLRTTADTFCKLFRVYNSFLRGKLYTGACRGD 165
 Db 161 LPEASAPLRTTFTVDTLCKLFRVYNSFLRGKLYTGACRGD 205

RESULT 9

AAS77874 PRELIMINARY; PRT; 206 AA;
 AC AAS77874
 DT 15-APR-2004 (TREMELrel. 27, Created)
 DT 15-APR-2004 (TREMELrel. 27, Last sequence update)
 DT 15-APR-2004 (TREMELrel. 27, Last annotation update)
 DE Erythropoietin
 OS Canis familiaris (Dog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.,
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY572971; AAS77874.1; -
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003013; EPO TPO.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 SQ SEQUENCE 206 AA; 22666 MW; 1BEC64A02CE4F5B0 CRC64;
 Query Match 81.9%; Score 693; DB 2; Length 206;
 Best Local Similarity 81.2%; Pred. No. 9.6e-58;
 Matches 134; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLELYLEAKAEENITTCGAHCSLNENITVPTKVNFKYAKMEVGQQA 60

Db 41 APPRLICDSRVLELYLEAKAEENITTCGAHCSLNENITVPTKVNFKYAKMEVGQQA 100
 QY 61 VEWGGLALSSAVLRGQALLVNSQWEPLOLHVYDKAVSLRSLTLLRALGAKREMS 120
 Db 101 LEVWGGLALSSAVLRGQALLVNSQWEPLOLHVYDKAVSLRSLTLLRALGAKREMS 160
 QY 121 PDAAASAPLRTTADTFCKLFRVYNSFLRGKLYTGACRGD 165
 Db 161 LPEASAPLRTTFTVDTLCKLFRVYNSFLRGKLYTGACRGD 205

RESULT 10

EPO_BOVIN STANDARD; PRT; 192 AA.
 ID EPO_BOVIN
 AC P48617;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 OS Bos taurus (Bovine)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Boran; TISSUE=Kidney;
 RX MEDLINE=96257233; PubMed=8666286;
 RA Suliman H.B., Majliva P.A.O., Feldman B.F., Mertens E.J.
 RL Logan-Henfrey L.H.;
 RT "Cloning of a cDNA encoding bovine erythropoietin and analysis of its transcription in selected tissues."
 RL Gene 171:275-280 (1996).
 CC -! FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocytes.
 CC -! SUBCELLULAR LOCATION: Secreted.
 CC -! TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
 CC -! SIMILARITY: Belongs to the EPO / TPO family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; L41354; AAB41268.1; -
 CC EMBL; U44762; AAB65653.1; -
 CC HSSP; P01588; 1CN4;
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR001323; EPO TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO TPO; 1.
 DR PIRSF; PIRSF001351; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 192 Erythropoietin.
 FT DISULFID 32 187 By similarity.
 FT DISULFID 54 58 By similarity.
 FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 63 63 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 192 AA; 21075 MW; DEC419022F7B483A CRC64;
 Query Match 81.9%; Score 692.5; DB 1; Length 192;
 Best Local Similarity 83.1%; Pred. No. 9.8e-58;

RESULT 7

RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21290682; PubMed=11396976;	
RA	Vilalta A., Wu D., Margalith M., Hobart P.;	
RA	"Rabbit EPO gene and cDNA: expression of rabbit EPO after	
RT	intramuscular injection of pDNA.,";	
RL	Biochem. Biophys. Res. Commun. 284:823-827(2001).	
DR	EMBL; AF290943; AAG36962.1; -	
DR	HSSP; P01588; 1CN4.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0005128; F:erythropoietin receptor binding; IEA.	
DR	GO; GO:0005179; F:hormone activity; IEA.	
DR	InterPro; IPR009079; 4_helix_cytokine.	
DR	InterPro; IPR001323; EPO_TPO.	
DR	InterPro; IPR003013; Erythroptn.	
DR	Pfam; PF00758; EPO_TPO; 1.	
DR	PfirsF; PIRSFO01951; EPO; 1.	
DR	PRINTS; PR00272; ERYTHROPTN.	
DR	PROSITE; PS00817; EPO_TPO; 1.	
DR	SEQUENCE 195 AA; 21025 MW; 1F1DC7F403A303EC CRC64;	
QY	Query Match 80.4%; Score 680.5; DB 2; Length 195;	
QY	Best Local Similarity 81.3%; Pred. No. 1.4e-56;	
QY	Matches 135; Conservative 12; Mismatches 18; Indels 1;	
DB	1 APPRLICDSRVLYRLVLEAKEARENITTCGAHCNSLNETVPTDKNPFYANKRMVE	
DB	29 APARLICDSRVLYRLVLEAKEARENVTGCAEGCSLGENITVPTDKYNFHHKKKSE	
QY	61 VEVWQGLALLSEAVLRQALLVNSQPEWPELQHVDKAVSGLSRLTTLRLALCAQK	
DB	89 VEVWQGLALLSEAMLRQALLVNSQQLPETLVHVDKAVSGLSRLTSLLRALGVQ	
QY	121 PDAA-SAAPLRTTATDFKLVVSNFRLGKLYTGACRTGD 165	
DB	143 PFERASSAAPLRTVAADTLCLFRIYSNFRGKLYTGACRRGD 194	
RESULT 14		
ID	Q9GKA3 PRELIMINARY; PRT; 195 AA.	
AC	Q9GKA3;	
DT	01-WAR-2001 (TRENBIrel. 16, Created)	
DT	01-WAR-2001 (TRENBIrel. 16, Last sequence update)	
DT	01-WAR-2004 (TRENBIrel. 26, Last annotation update)	
DE	Erythropoietin.	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
NCBI	TaxID=9986;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21290682; PubMed=11396976;	
RA	Vilalta A., Wu D., Margalith M., Hobart P.;	
RA	"Rabbit EPO gene and cDNA: expression of rabbit EPO after	
RT	intramuscular injection of pDNA.,";	
RL	Biochem. Biophys. Res. Commun. 284:823-827(2001).	
DR	EMBL; AF290943; AAG36961.1; -	
DR	PIR; JC7699; JC7699.	
DR	HSSP; P01588; 1CN4.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0005128; F:erythropoietin receptor binding; IEA.	
DR	GO; GO:0005179; F:hormone activity; IEA.	
DR	InterPro; IPR009079; 4_helix_cytokine.	
DR	InterPro; IPR001323; EPO_TPO.	
DR	InterPro; IPR003013; Erythroptn.	
DR	Pfam; PF00758; EPO_TPO; 1.	
DR	PfirsF; PIRSFO01951; EPO; 1.	
DR	PRINTS; PR00272; ERYTHROPTN.	
DR	PROSITE; PS00817; EPO_TPO; 1.	
DR	SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;	
QY	Query Match 80.4%; Score 680.5; DB 2; Length 195;	
QY	Best Local Similarity 81.3%; Pred. No. 1.4e-56;	

Matches 138; Conservative 8; Mismatches 19; Indels 1; Gaps 1;
 QY 1 APPRLICDSRVLYLEAEAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 60
 DB 26 APARLICDSRVLYLEAEAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 85
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRLALGAKKEAIS 120
 DB 86 LEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRLALGAKKEAIS 145
 QY 121 PPDAA-SAAPLRITATDTKFLFRVYSNFRGLKLYTGEACRTGD 165
 DB 146 LPDATPSAPLRAFTVDALSKLFRIYSNFRGLKLYTGEACRTGD 191
 RESULT 11
 EPO_MOUSE
 ID EPO_MOUSE STANDARD; PRT; 192 AA.
 AC P07321.
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=67039105; PubMed=3773894;
 RX Shoemaker C.B., Mitsuoka L.D.:
 RA "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RT Mol. Cell. Biol. 6:849-859 (1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=67039104; PubMed=3022133;
 RX McDonald J.D., Lin F.-K., Goldwasser E.:
 RA "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RT Mol. Cell. Biol. 6:842-848 (1986).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riener C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Chung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.:
 RA "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RT Nucleic Acids Res. 29:1352-1365 (2001).
 RN [4]
 RN SEQUENCE OF 1-52 FROM N.A.
 RP STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Christen S., Duprez V., Macouche L., Gisselbrecht S., Mayeux P.,
 RA Labombard C.:
 RA "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythrocytosis 1W32 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999 (1997).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M12482; AAA37568.1; --
 DR EMBL; M12930; AAA37570.1; --
 DR EMBL; AF312033; AAK28825.1; --
 DR EMBL; Y11971; CAA72707.1; --
 DR PIR; A24902; A24902.
 DR HSSP; P01588; 1CN4.
 DR MGD; MGI:95407; Epo.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT CARBOHYD 50 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;
 Query Match 81.48; Score 689; DB 1; Length 192;
 Best Local Similarity 80.08; Pred. No. 2.1e-57;
 Matches 132; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYLEAEAEENITTCABHCSLNENITVPDTKVFYAKRMEVQQA 60
 DB 27 APARLICDSRVLYLEAEAEENITTCABHCSLNENITVPDTKVFYAKRMEVEQA 86
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRLALGAKKEAIS 120
 DB 87 LEVWQGLALLSEAVLRGQALLVNSQWPEPLQHVDKAVSGLSLTLRLALGAKKEAIS 146
 QY 121 PPDAA-SAAPLRITATDTKFLFRVYSNFRGLKLYTGEACRTGD 165
 DB 147 PPDTPPAPLRITLTVDFCKLFRVYANFRGLKLYTGEACRTGD 191
 RESULT 12
 EPO_SHEEP
 ID EPO_SHEEP STANDARD; PRT; 194 AA.
 AC P33709; Q28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.:
 RA "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116 (1993).
 RN [2]
 RN SEQUENCE OF 4-194 FROM N.A.
 RP TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status experimental
F;34-188,56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 60
DB 28 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 147

QY 121 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 165
DB 148 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 192

RESULT 2
JQ0173
A;Description: precursor - crab-eating macaque
C;Species: Macaca fascicularis (Crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: JQ0173
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A;Reference number: JQ0173; MUID:87055236; PMID:2877922
A;Accession: JQ0173
A;Molecule type: mRNA
A;Residues: 1-192 <LIN>
A;Cross-references: UNIPROT:P07865; GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:g342
A;Experimental source: kidney
C;Comment: This protein is the principal hormone involved in the regulation of erythrocy
C;Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Superfamily: erythropoietin
A;Description: the primary inducer of erythrocyte formation
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 84.5; DB 1; Length 192;
Best Local Similarity 91.5%; Pred. No. 1.1e-65;
Matches 151; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 60
DB 28 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 146

QY 121 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 165
DB 147 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 191

RESULT 3
184613
erythropoietin precursor - rhesus macaque

A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 713; DB 1; Length 188;
Best Local Similarity 84.2%; Pred. No. 8.8e-61;
Matches 139; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 60
DB 23 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 82

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I84613
R;Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homol
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I84613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192 <RES>
A;Cross-references: UNIPROT:Q28513; GB:L10609; NID:G342095; PIDN:AAA36842.1; PID:G34209;
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver
C;Function:
A;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoietin #status predicted <MAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.8%; Score 759.5; DB 1; Length 192;
Best Local Similarity 90.3%; Pred. No. 3.2e-65;
Matches 149; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 60
DB 28 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVDAKVGSLRSLTLLRALGAQKEAIS 146

QY 121 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 165
DB 147 PPDAASAPLRITITADTRFKLFRVYSNFRGLKLYTGACRTGD 191

RESULT 4
I46083
erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 18-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
R;Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homol
A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Accession: I46083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-188 <MEN>
A;Cross-references: UNIPROT:P33708; GB:L10606; NID:G163820; PIDN:AAA30807.1; PID:G16382
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver
C;Function:
A;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 713; DB 1; Length 188;
Best Local Similarity 84.2%; Pred. No. 8.8e-61;
Matches 139; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 60
DB 23 APPRLCDSRVLYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGOQA 82

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:09:33 ; Search time 12.9607 Seconds
(without alignments)
1224.913 Million cell updates/sec

Title: US-10-780-297-1
Perfect score: 846
Sequence: 1 APPRLCDSRVLYRYLEAY.....SNFLRGKLYTGCACTGTD 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	846	100.0	193	1	ZURU	erythropoietin pre
2	764.5	90.4	192	1	JQ0173	erythropoietin pre
3	759.5	89.8	192	1	I84613	erythropoietin pre
4	713	84.3	188	1	I46083	erythropoietin pre
5	701	82.9	192	1	S28148	erythropoietin pre
6	685.5	81.0	194	1	I46401	erythropoietin pre
7	681	80.5	192	1	A24902	erythropoietin pre
8	680.5	80.4	195	2	JC7699	erythropoietin - r
9	678	80.1	190	2	I46578	erythropoietin - p
10	638	75.4	175	2	I46199	erythropoietin - d
11	90	10.6	353	2	G02729	erythropoietin - h
12	89	10.5	353	2	I80105	thrombopoietin pre
13	88	10.4	353	2	AB0323	thrombopoietin pre
14	87.5	10.3	346	2	AE0359	ribonucleoside-dip
15	86	10.2	286	2	AS5530	Solute binding rec
16	83	9.8	296	2	AI0443	megakaryocyte grow
17	83	9.8	339	2	A83274	probable 2-hydroxy
18	80.5	9.5	3033	1	GNVJ78	UDP-N-acetylpyruvo
19	79.5	9.4	1829	2	T35681	genome polyprotein
20	79	9.3	480	2	S56639	probable sensory h
21	78.5	9.3	813	2	AF0526	ribosomal protein
22	78.5	9.3	897	2	AS4696	ATP-dependent heli
23	78	9.2	348	2	T35450	EGF receptor subst
24	78	9.2	455	2	AG2919	ABC transporter AT
25	78	9.2	455	2	H97693	conserved hypotet
26	78	9.2	747	1	S36741	methylamine utiliz
27	77.5	9.2	242	2	AD1928	probable copper-tr
28	77	9.1	451	2	S75569	hypothetical prote
29	76.5	9.0	154	2	H82810	bacterioferritin X

30	76.5	9.0	425	2	AE3465	mandelate racemase
31	75.5	8.9	637	2	S75772	hypothetical prote
32	74.5	8.8	400	2	AB2922	conserved hypotet
33	74.5	8.8	425	2	C97696	ITS beta (AF305057
34	74.5	8.8	824	2	D64738	ATP-dependent heli
35	74	8.7	282	2	B37994	RF2 protein - salm
36	74	8.7	326	2	JC4125	thrombopoietin pre
37	74	8.7	335	2	AH3825	ribonucleoside-dip
38	74	8.7	1564	2	S55317	probable transport
39	73.5	8.7	401	2	H83911	hypothetical prote
40	73.5	8.7	476	1	S71789	GCNS protein - hum
41	73.5	8.7	717	2	F82613	VacB protein XF198
42	73	8.6	263	2	B75361	WD-repeat family p
43	73	8.6	1089	2	S53978	PSE1 protein - yea
44	72.5	8.6	379	2	H69478	NADH2 dehydrogenas
45	72.5	8.6	401	2	AF3341	precorrin-6y C5,15

ALIGNMENTS

RESULT 1

ZURU

erythropoietin precursor [validated] - human

C/Species: Homo sapiens (man)

C/Date: 27-Nov-1985 #sequence, revision 27-Nov-1985 #text_change 09-Jul-2004

C/Accession: A01855; A24744; A25384; A22210; S56178

R/Jacobs, K.; Shoemaker, C.; Ruderstorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810, 1985

A/Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet

A/Reference number: A01855; MUID:85137899; PMID:3838366

A/Accession: A01855

A/Molecule type: mRNA; DNA

A/Residues: 1-193 <JAC>

A/Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R/Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrise, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A/Title: Cloning and expression of the human erythropoietin gene.

A/Reference number: A24744; MUID:86067948; PMID:3865178

A/Accession: A24744

A/Molecule type: DNA

A/Residues: 1-193 <LIN>

A/Cross-references: GB:M1319; NID:gl82197; PIDN:AA52400.1; PID:gl82198

R/Bai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A/Title: Structural characterization of human erythropoietin.

A/Reference number: A25384; MUID:86140080; PMID:3949763

A/Accession: A25384

A/Molecule type: protein

A/Residues: 28-86,'Q',87-193 <LAI>

A/Experimental source: urine

A/Note: Forms without the carboxyl-terminal residue and the four carboxyl-terminal resi

R/Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A/Title: Isolation of human erythropoietin with monoclonal antibodies.

A/Reference number: A22210; MUID:94135751; PMID:6698989

A/Accession: A22210

A/Molecule type: protein

A/Residues: 28-29,'X',31-33,'L',35-50,'X',52-53,'D',55,'G',57 <YAN>

R/Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A/Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured

A/Reference number: S56178; MUID:95284365; PMID:7766897

A/Accession: S56178

A/Molecule type: protein

A/Residues: 28-33,'X',35-37 <MTS>

C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver

C/Genetics: GDB:EP0

A/Gen: GDB:EP0

A/Cross-references: GDB:119110; OMIM:133170

A/Map position: 7q31.3-7q22.1

A/Introns: 5/1; 53/3; 82/3; 142/3

C/Function:

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 14

US-10-410-913-73
; Sequence 73, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-913-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAWKRMVEGQQA 60
Db 1 APPLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAWKRMVEGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 15

US-10-706-701-1
; Sequence 1, Application US/10706701
; Publication No. US20040209802A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Paul
; APPLICANT: Roeddiger, Ralf
; APPLICANT: Walter-Matsui, Ruth
; TITLE OF INVENTION: TREATMENT OF DISTURBANCES OF IRON DISTRIBUTION
; FILE REFERENCE: 21435

; CURRENT APPLICATION NUMBER: US/10/706,701
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 02026342.2
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-701-1

Query Match 100.0%; Score 846; DB 17; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAWKRMVEGQQA 60
Db 1 APPLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAWKRMVEGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

Search completed: December 3, 2004, 13:41:15
Job time : 51.8459 secs

; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-410-930-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
DB 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGD 165

RESULT 12
US-10-410-997-73
; Sequence 73, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Catlyn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-410-997-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
DB 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGACRTGD 165

RESULT 13
US-10-411-012-73
; Sequence 73, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Catlyn
; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-411-012-73

Query Match 100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
DB 1 APRRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDKAVSGLSRLTTLRALGAQKEAIS 120

```
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-73

Query Match      100.0%; Score 846; DB 15; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
DB 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 9
US-10-411-049-73
; Sequence 73, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; PRIOR FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-411-049-73

Query Match      100.0%; Score 846; DB 15; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
DB 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 10
US-10-634-477-1
; Sequence 1, Application US/10634477
; Publication No. US20040110679A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Paul
; APPLICANT: Roeddiger, Ralf
; APPLICANT: Walter-Matsui, Ruth
; TITLE OF INVENTION: TREATMENT OF DISTURBANCES OF IRON DISTRIBUTION
; FILE REFERENCE: 21368
; CURRENT APPLICATION NUMBER: US/10/634,477
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 02019100.3
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-634-477-1

Query Match      100.0%; Score 846; DB 16; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
DB 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKNFYAWKRMVEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVDRKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGD 165

RESULT 11
US-10-410-930-73
; Sequence 73, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
```

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165

RESULT 6

US-10-411-037-73
; Sequence 73, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-73

Query Match 100.0%; Score 846; DB 15; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165

RESULT 7

US-10-411-026-73

Sequence 73, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-73

Query Match 100.0%; Score 846; DB 15; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLELYLLEAKEAENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
DB 121 PPDASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165

RESULT 8

US-10-410-962-73
; Sequence 73, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692

RESULT 2
US-09-945-517-1
; Sequence 1, Application US/09945517
; Publication No. US20030104996A1
; GENERAL INFORMATION:
; APPLICANT: Li, Tiansheng
; APPLICANT: Chang, Byeong
; APPLICANT: Sloey, Christopher
; TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
; FILE REFERENCE: A-803
; CURRENT APPLICATION NUMBER: US/09/945,517
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-517-1

Query Match 100.0%; Score 846; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165

RESULT 3
US-10-014-363-1
; Sequence 1, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Bug, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-1

Query Match 100.0%; Score 846; DB 13; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165

RESULT 4
US-10-241-356-1
; Sequence 1, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-1

Query Match 100.0%; Score 846; DB 14; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
DB 1 APPRLCDRVLRYLLEAKAEENITTCGAHCSLNENITVPDTKVFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGLKLYTGEACRTGD 165

RESULT 5
US-10-293-551-1
; Sequence 1, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-1

Query Match 100.0%; Score 846; DB 14; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.9e-85;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:28:44 ; Search time 50.8459 Seconds
(without alignments)
1157.277 Million cell updates/sec

Title: US-10-780-297-1
Perfect score: 846
Sequence: 1 APPRLICDSRVLYRLLLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	9	US-09-853-731-1
2	846	100.0	165	10	US-09-945-517-1
3	846	100.0	165	13	US-10-014-363-1
4	846	100.0	165	14	US-10-241-356-1
5	846	100.0	165	15	US-10-293-551-1
6	846	100.0	165	15	US-10-411-037-73
7	846	100.0	165	15	US-10-411-026-73
8	846	100.0	165	15	US-10-410-962-73
9	846	100.0	165	15	US-10-411-049-73
10	846	100.0	165	16	US-10-634-477-1
11	846	100.0	165	16	US-10-410-930-73
12	846	100.0	165	16	US-10-410-997-73
13	846	100.0	165	16	US-10-411-012-73

14	846	100.0	165	16	US-10-410-913-73
15	846	100.0	165	17	US-10-706-701-1
16	846	100.0	166	9	US-09-853-731-2
17	846	100.0	166	13	US-10-014-363-2
18	846	100.0	166	14	US-10-241-356-2
19	846	100.0	166	14	US-10-293-551-2
20	846	100.0	166	14	US-10-400-377-2
21	846	100.0	166	14	US-10-400-708-2
22	846	100.0	166	14	US-10-298-148-2
23	846	100.0	166	15	US-10-360-101-227
24	846	100.0	166	15	US-10-467-115-1
25	846	100.0	166	16	US-10-658-834A-201
26	846	100.0	166	16	US-10-774-149-2
27	846	100.0	166	16	US-10-774-149-2
28	846	100.0	166	16	US-10-468-496-133
29	846	100.0	166	17	US-10-773-654-2
30	846	100.0	166	17	US-10-866-540-2
31	846	100.0	169	13	US-10-014-363-4
32	846	100.0	174	13	US-10-014-363-5
33	846	100.0	174	13	US-10-014-363-5
34	846	100.0	193	10	US-09-813-775C-4
35	846	100.0	193	14	US-10-113-824-2
36	846	100.0	193	16	US-10-612-665-10
37	846	100.0	193	16	US-10-612-665-22
38	846	100.0	193	16	US-10-612-665-112
39	846	100.0	193	17	US-10-676-694-10
40	846	100.0	193	17	US-10-676-694-22
41	846	100.0	193	17	US-10-676-694-112
42	846	100.0	209	14	US-10-230-454-4
43	846	100.0	220	14	US-10-196-183-2
44	846	100.0	370	14	US-10-230-454-3
45	846	100.0	428	14	US-10-435-608-10

ALIGNMENTS

RESULT 1
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0.
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match	100.0%;	Score	846;	DB	9;	Length	165;
Best Local Similarity	100.0%;	Pred. No.	1.9e-85;	Indels	0;	Gaps	0;
Matches	165;	Conservative	0;	Mismatches	0;		
QY	1	APPRLICDSRVLYRLLLEAKEAENITTCBAEHC	SLNENITVPDTKVNFWAKRMEVQQA	60			
Db	1	APPRLICDSRVLYRLLLEAKEAENITTCBAEHC	SLNENITVPDTKVNFWAKRMEVQQA	60			
QY	61	VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSITLLRALGAKQKAIS	120				
Db	61	VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSITLLRALGAKQKAIS	120				
QY	121	PDAAASAPLTIITADTFKLFVYSNPLRGLKLYTGEACRTGD	165				
Db	121	PDAAASAPLTIITADTFKLFVYSNPLRGLKLYTGEACRTGD	165				

REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34

Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 1.4e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 233 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 120
Db 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 352
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
Db 353 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 397

RESULT 14
US-08-809-156B-34
Sequence 34, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Aesada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Ueno, Takashi
APPLICANT: Koyama, No. 6472204auto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-34

Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 1.4e-98;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 233 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 120
Db 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 352
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
Db 353 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 397

RESULT 15
US-09-552-265B-2
Sequence 2, Application US/09552265B
Patent No. 6555343
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederick
APPLICANT: Henner, Dennis, J.
TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
FILE REFERENCE: GENENT 057CPI
CURRENT APPLICATION NUMBER: US/09/552,265B
CURRENT FILING DATE: 2000-04-19
PRIORITY APPLICATION NUMBER: US 09/307307
PRIORITY FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Pan troglodytes
US-09-552-265B-2

Query Match 99.1%; Score 838; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 1.8e-98;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
Db 28 APPRLICDSRVLEKAEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHLVDKAVSGLSLITLLRALGAKAEIS 147
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 165
Db 148 PPDAASAAPLRTITADTFKLFVYSNFRGKLYTGEACRTGD 192

Search completed: December 3, 2004, 13:39:27
Job time : 19.9426 secs

Db 28 APRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 165
Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 192

RESULT 11
US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; FILE REFERENCE: GENENT.057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; PRIOR FILING DATE: 2000-04-19
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-265B-4

Query Match 100.0%; Score 846; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAKRMEVGGQA 60
Db 28 APRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 165
Db 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 192

RESULT 12
US-09-554-451-8
; Sequence 8, Application US/09554451
; Patent No. 6680207
; GENERAL INFORMATION:
; APPLICANT: Jonathan Paul MURPHY
; APPLICANT: Anthony ATKINSON
; TITLE OF INVENTION: Detection of Molecules in Samples
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/554,451

FILING DATE: 15-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/03449
; FILING DATE: No. 6680207ember 16, 1998
; APPLICATION NUMBER: GB 9723955.2
; FILING DATE: No. 6680207ember 14, 1997
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8
Query Match 99.6%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 3.3e-99;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAKRMEVGGQA 60
Db 1 APRLICDSRVLELYLEAKEAENITTCGAHCSLNENITVPTDKVNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGD 165

RESULT 13
US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asado, Kiyozo
; APPLICANT: Umori, Takashi
; APPLICANT: Ueno, Takashi
; APPLICANT: Koyama, No. 6426042uto
; APPLICANT: Hashino, Kimikazu
; APPLICANT: Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2800
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-37

Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-99; Mismatches 0; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAWKMEVGGQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAWKMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSRLTLLRALGAKQKAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSRLTLLRALGAKQKAIS 120
QY 121 PDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRTGD 165
DB 121 PDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRTGD 165

RESULT 9
US-07-903-220-1
Sequence 1, Application US/07903220
Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1176
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-903-220-1
Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAWKMEVGGQA 60
DB 28 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAWKMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSRLTLLRALGAKQKAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDKAVSGLSRLTLLRALGAKQKAIS 147
QY 121 PDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRTGD 165
DB 148 PDAASAAPLRTITADTFKLFVYSNFLRGKLYTGEACRTGD 192

RESULT 10
US-08-883-795A-34
Sequence 34, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcove, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-795A-34

Query Match 100.0%; Score 846; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFYAWKMEVGGQA 60

```
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 100.0%; Score 846; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLCDSRVRLRYLLEAKENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 1 APRRLCDSRVRLRYLLEAKENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 6
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLCDSRVRLRYLLEAKENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 1 APRRLCDSRVRLRYLLEAKENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGD 165

RESULT 8
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3924
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-1

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165

RESULT 3

US-09-830-967-1
; Sequence 1, Application US/09830967
; Patent No. 677205
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165

RESULT 4

US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)883-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-70

Query Match 100.0%; Score 846; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKAEENITTCBAEHCNSINENITVPDTKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165
DB 121 PPDAASAAPLRTITADTFRKLFVYNSFLRGKLYTGACRTGD 165

RESULT 5

US-09-604-871-2

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:23:08 ; Search time 18.9426 Seconds
(without alignments)
577.665 Million cell updates/sec

Title: US-10-780-297-1
Perfect score: 846
Sequence: 1 APPRLCDSRVLEYLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	846	100.0	165	3	US-09-604-871-1
2	846	100.0	165	4	US-09-604-938-1
3	846	100.0	165	4	US-09-830-967-1
4	846	100.0	166	1	US-08-318-193-70
5	846	100.0	166	3	US-09-604-871-2
6	846	100.0	166	4	US-09-604-938-2
7	846	100.0	166	4	US-09-462-941-2
8	846	100.0	166	5	PCT-US94-04361-37
9	846	100.0	133	1	US-07-903-220-1
10	846	100.0	133	2	US-08-883-795A-34
11	846	100.0	193	4	US-09-552-265B-4
12	843	99.6	165	4	US-09-554-451-8
13	843	99.6	412	4	US-09-366-009-34
14	843	99.6	412	4	US-08-809-156B-34
15	838	99.1	193	4	US-09-552-265B-2
16	834	98.6	193	4	US-09-552-265B-5
17	830	98.1	166	5	PCT-US94-04361-45
18	825	97.5	166	4	US-09-552-265B-30
19	825	97.5	193	4	US-09-552-265B-46
20	824	97.4	166	4	US-09-552-265B-22
21	824	97.4	166	4	US-09-552-265B-32
22	824	97.4	193	4	US-09-552-265B-38
23	824	97.4	193	4	US-09-552-265B-48
24	822	97.2	166	4	US-09-552-265B-20
25	822	97.2	166	4	US-09-552-265B-24
26	822	97.2	193	4	US-09-552-265B-36
27	822	97.2	193	4	US-09-552-265B-40

28 821 97.0 166 4 US-09-552-265B-26 Sequence 26, Appl
29 821 97.0 166 4 US-09-552-265B-31 Sequence 31, Appl
30 821 97.0 193 4 US-09-552-265B-42 Sequence 42, Appl
31 821 97.0 193 4 US-09-552-265B-47 Sequence 47, Appl
32 820 96.9 166 4 US-09-552-265B-18 Sequence 18, Appl
33 820 96.9 166 4 US-09-552-265B-23 Sequence 23, Appl
34 820 96.9 166 4 US-09-552-265B-28 Sequence 28, Appl
35 820 96.9 166 4 US-09-552-265B-33 Sequence 33, Appl
36 820 96.9 193 4 US-09-552-265B-34 Sequence 34, Appl
37 820 96.9 193 4 US-09-552-265B-39 Sequence 39, Appl
38 820 96.9 193 4 US-09-552-265B-44 Sequence 44, Appl
39 820 96.9 193 4 US-09-552-265B-49 Sequence 49, Appl
40 818 96.7 166 4 US-09-552-265B-21 Sequence 21, Appl
41 818 96.7 166 4 US-09-552-265B-25 Sequence 25, Appl
42 818 96.7 193 4 US-09-552-265B-37 Sequence 37, Appl
43 818 96.7 193 4 US-09-552-265B-41 Sequence 41, Appl
44 817 96.6 166 4 US-09-552-265B-27 Sequence 27, Appl
45 817 96.6 193 4 US-09-552-265B-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-604-871-1
; Sequence 1, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josele, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-1
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.4e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPRLCDSRVLEYLEAKEENITTCGAHCSLNENITVPDTKNFVAKMEYGOQA 60
Db 1 APPRLCDSRVLEYLEAKEENITTCGAHCSLNENITVPDTKNFVAKMEYGOQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSSQFWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSSQFWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGEACRTGD 165
RESULT 2
US-09-604-938-1
; Sequence 1, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

This Page Blank (uspto)

Db 61 VEVQGLALLSEAVLRGQALLVNSSQWEPLOHVDKAVSGLRSLTLLRALGAQKEAIS 120
Qy 121 PPDASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTFRKLFVYNSFLRGKLYTGEACRTGD 165

Search completed: December 3, 2004, 13:34:05
Job time : 65.3112 secs

Db 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHVVDKAVSGRLSLTTLRALGAQKEAIS 120
 QY 121 PPDASAAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
 Db 121 PPDASAAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 12
 ADL06780
 ID ADL06780 standard; protein; 165 AA.
 AC ADL06780;
 DT 03-JUN-2004 (first entry)
 DE Human 165 residue erythropoietin (EPO), SEQ ID NO:1.
 XX Human; erythropoietin; EPO; iron distribution disturbance; diabetes;
 KW non-insulin dependent diabetes; type 2 diabetes; reticulocyte production;
 KW red blood cell production; antidiabetic.
 XX Homo sapiens.
 OS
 PN WO2004019972-A1.
 XX
 PD 11-MAR-2004.
 XX
 XX 20-AUG-2003; 2003WO-EP009194.
 XX
 XX 29-AUG-2002; 2002EP-00019100.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Lehmann P, Rosediger R, Walter-Matsui R;
 PI WPI; 2004-282643/26.
 XX
 XX Use of erythropoietin protein in manufacture of medicament for treating
 PT disturbances of iron distribution in diabetes.
 PT
 XX Claim 6; SEQ ID NO 1; 31pp; English.

The invention relates to the use of an erythropoietin (EPO) protein for the treatment of disturbances of iron distribution in diabetes. The erythropoietin protein is preferably a human erythropoietin (e.g., epoetin alpha and epoetin beta) which may be expressed by endogenous gene activation or an erythropoietin analogue such as darbepoietin alpha. The erythropoietin protein used in the method may also be modified by the addition of 1-6 glycosylation sites, or by pegylation. Patients with diabetes have been found to have a high probability of being affected by disturbances of iron distribution. In such patients, the overall concentration of iron in the body is normal (compared with conditions such as anaemia), but the individual may suffer the effects of iron accumulation in certain organs, leading to organ damage and destruction, and/or experience effects similar to anaemia due to iron usage in blood cell formation being impaired. Erythropoietin causes bone marrow cells to increase production of reticulocytes and red blood cells, and this has been found to have a beneficial effect on iron distribution disturbances in diabetes e.g., non-insulin dependent (type 2) diabetes. Erythropoietin proteins may therefore be used to manufacture a medicament for the treatment of disturbances of iron distribution in diabetes. The present sequence represents a 165 amino acid human erythropoietin which is specifically claimed for use in the invention.

XX Sequence 165 AA;
 SQ

Query Match 100.0%; Score 846; DB 8; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNNITVPTDKVNFYAKRMEVGGQA 60
 |||||

Db 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNNITVPTDKVNFYAKRMEVGGQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHVVDKAVSGRLSLTTLRALGAQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSSQWPEPLQHVVDKAVSGRLSLTTLRALGAQKEAIS 120
 QY 121 PPDASAAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
 Db 121 PPDASAAAPLRTITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 13
 ADN49745
 ID ADN49745 standard; protein; 165 AA.
 AC ADN49745;
 DT 15-JUL-2004 (first entry)
 DE Mature human erythropoietin protein SeqID 73.
 XX human; erythropoietin; EPO; glycoconjugation; glycoPEGylated EPO peptide;
 KW anaemia; antianaemic; haematocrit level; kidney dialysis; haematology;
 KW erythropoietin.
 XX Homo sapiens.
 OS
 PN WO2004033651-A2.
 XX
 PD 22-APR-2004.
 XX
 XX 08-OCT-2003; 2003WO-US031974.
 XX
 XX 09-OCT-2002; 2002WO-US032263.
 PR 05-NOV-2002; 2002US-00287994.
 PR 06-JAN-2003; 2003US-00360770.
 PR 19-FEB-2003; 2003US-00360779.
 PR 09-APR-2003; 2003US-00410945.
 XX
 XX (NEOS-) NEOSE TECHNOLOGIES INC.
 XX
 XX De Freses S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
 PI WPI; 2004-399848/37.
 XX
 XX Novel erythropoietin peptide comprising one or more glycans, having
 PT glycoconjugate molecule covalently attached to peptide, useful for
 PT treating anemia in mammal such as human.
 XX
 XX Claim 38; SEQ ID NO 73; 1019pp; English.

This invention relates to novel erythropoietin (EPO) peptides and the remodelling and glycoconjugation of these naturally occurring peptides thereof. Specifically, each EPO peptide comprises one or more glycans and has a glycoconjugate molecule such as polyethylene glycol (PEG) attached to it. Accordingly, the present invention provides glycoPEGylated EPO peptides that have either monoantennary, biantennary or triantennary glycans covalently attached thereto. As such, these peptides are useful for the treatment of anaemia, and hence exhibit antianaemic activities working to increase haematocrit levels in mammals, in particular in humans i.e. increasing the relative volume of blood occupied by erythrocytes. Furthermore, EPO therapy can be used to treat kidney dialysis patients. This polypeptide is a human protein sequence related to the field of haematology, given in an exemplification of the invention.

XX Sequence 165 AA;
 SQ

Query Match 100.0%; Score 846; DB 8; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNNITVPTDKVNFYAKRMEVGGQA 60
 |||||

QY 121 PPDAASAPLETITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAPLETITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 10
ABP98492
ID ABP98492 standard; protein; 165 AA.

AC ABP98492;
XX
XX 29-JUL-2003 (first entry)
XX
XX Amino acid sequence of human erythropoietin (EPO).
DE Human; erythropoietin; EPO; novel erythropoiesis stimulating protein;
KW NESF; haemocrit level.
XX
XX Homo sapiens.

OS
XX WO2003020299-A1.
XX
XX 13-MAR-2003.
XX
XX 29-AUG-2002; 2002WO-US027855.
XX
XX 30-AUG-2001; 2001US-00945517.
XX
XX (KIRI) KIRIN AMGEN INC.

XX
XX Li T, Chang BS, Sloey C;
XX
XX WPI; 2003-402847/38.

XX
XX Pharmaceutical formulation for single use comprises biologically active
PT agent, methionine and optional preservative and does not contain human
PT serum albumin.

XX
XX Claim 6; Page 37; 40pp; English.

XX
XX The present sequence represents human erythropoietin (EPO). EPO is used
CC as the active agent in formulations of the invention. The specification
CC describes a pharmaceutical formulation, which comprises a biologically
CC active agent (e.g. EPO or novel erythropoiesis stimulating protein
CC (NESP)), methionine and a preservative. The formulation does not contain
CC human serum albumin (HSA). The formulation has improved stability.
CC Incorporation of methionine and other stabilizing agents into the
CC formulation produces a more stable formulation, even in extreme
CC conditions, where the critical degradations induced by light, heat,
CC impurities in additives, leacheates in the prefilled syringes, the
CC manufacturing process, storage, transportation and handling are
CC prevented. The formulation is useful as a single use and a multi-dose
CC formulation. Where NESP is the active agent, it may be used to raise
CC haemocrit levels

XX
XX Sequence 165 AA;
Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLTLRALGAQKEAIS 120

QY 121 PPDAASAPLETITADTFKRLFRVYSNFRGKLYTGEACRTGD 165
DB 121 PPDAASAPLETITADTFKRLFRVYSNFRGKLYTGEACRTGD 165

RESULT 11
ABR39995
ID ABR39995 standard; protein; 165 AA.

XX
XX ABR39995;
XX
XX 02-SEP-2003 (first entry)
XX
XX Human erythropoietin (EPO) sequence.
DE
XX
XX EPO; erythropoietin; mutein; reticulocyte; red blood cell; antianemic;
KW AIDS; cancer.
XX
XX Homo sapiens.

XX
XX Key Location/Qualifiers
FH Disulfide-bond 7..161
FT /note= "disulphide bridge"
FT Disulfide-bond 29..33
FT /note= "disulphide bridge"
FT Modified-site 38
FT /note= "Asn is N-glycosylated"
FT Modified-site 83
FT /note= "Asn is N-glycosylated"
FT Modified-site 126
FT /note= "Ser is O-glycosylated"

XX
XX WO2003029291-A2.

XX
XX 10-APR-2003.

XX
XX 20-SEP-2002; 2002WO-EP010556.

XX
XX 25-SEP-2001; 2001EP-00122555.

XX
XX (HOPF) HOPFMANN LA ROCHE & CO AG F.

XX
XX Tischer W;

XX
XX WPI; 2003-457226/43.

XX
XX Novel erythropoietin mutein having in vivo biological activity of causing
PT bone marrow cells to increase production of reticulocytes/red blood
PT cells, is N-glycosylated at Asn38 and Asn83 but not N-glycosylated at
PT Asn24.

XX
XX Claim 6; Page 21-22; 22pp; English.

XX
XX The invention relates to an erythropoietin mutein (I) having the in vivo
CC biological activity of causing bone marrow cells to increase production
CC of reticulocytes and red blood cells, characterized by being N-
CC glycosylated at Asn38 and Asn83 but not N-glycosylated by being N-
CC an aqueous composition comprising an erythropoietin mutein is useful for
CC the preparation of a medicament for the treatment or prophylaxis of
CC diseases correlated with anemia in chronic renal failure patients (CRF),
CC AIDS and for the treatment of cancer patients undergoing chemotherapy.

XX
XX (I) or the composition is useful for treating a human patient
CC experiencing blood disorders characterized by low or defective red blood
CC cell production. (I) is useful for enhancing red blood cell formation.
XX The present sequence represents a human erythropoietin (EPO) sequence

XX
XX Sequence 165 AA;

Query Match 100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLTLRALGAQKEAIS 120

FT Disulfide-bond 7. .161
 FT Modified-site 24
 FT FT /note= "N-glycosylated"
 FT Disulfide-bond 29. .33
 FT FT /note= "N-glycosylated"
 FT Modified-site 38
 FT FT /note= "N-glycosylated"
 FT Modified-site 83
 FT FT /note= "N-glycosylated"
 FT Modified-site 126
 FT FT /note= "O-glycosylated"
 XX
 XX WO200187329-A1.
 XX
 XX 22-NOV-2001.
 XX
 XX 08-MAY-2001; 2001WO-EP005187.
 XX
 XX 15-MAY-2000; 2000EP-00110355.
 XX
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Papadimitriou A;
 PI
 XX WPI; 2002-082943/11.
 XX
 XX Composition useful in the treatment of e.g. AIDS comprises an
 PT erythropoietin protein, and a multiple charged inorganic anion in a
 PT buffer.
 PT
 XX Claim 28; Fig 1; 64pp; English.
 XX
 XX The invention relates to liquid pharmaceutical compositions comprising an
 CC erythropoietin (EPO) protein, a multiple negatively charged inorganic
 CC anion in a buffer which maintains the pH of the solution from 5.5-7.0,
 CC and optionally at least one excipient. The erythropoietin used in the
 CC composition is preferably human (AAM53061 or AAM53062) a human
 CC erythropoietin variant containing additional glycosylation sites
 CC (AAM53064-AAM53107), or an erythropoietin with the C-terminal addition of
 CC a C-terminal fragment of human chorionic gonadotropin (AAM53063).
 CC Erythropoietin is a glycoprotein essential for the formation of red blood
 CC cells and is therefore useful in the treatment of blood disorders
 CC characterised by low or defective red blood cell production. The
 CC compositions of the invention can be used in the treatment and prevention
 CC of anaemia in chronic renal failure patients (CRF), AIDS (acquired
 CC immunodeficiency syndrome), and/or for the treatment of cancer patients
 CC undergoing chemotherapy. Unlike prior art erythropoietin compositions,
 CC the compositions of the invention do not contain human serum albumin
 CC (thereby avoiding the possibility of viral infections and allergic
 CC reactions associated with this component), are liquid rather than
 CC lyophilisates (and therefore do not need to be reconstituted before
 CC administration), and are stable at elevated temperatures such as 25
 CC degrees Celsius and even 40 degrees Celsius, and therefore can be stored
 CC without refrigeration for prolonged periods without degradation and loss
 CC of activity. The present sequence represents the 165 residue form of
 CC human erythropoietin which is specifically claimed for use in a
 CC composition of the invention
 XX
 XX SQ Sequence 165 AA;
 Query Match 100.0%; Score 846; DB 5; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 DB 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPFLQHVDAKVSGLRSLTTLRALGAKQKALS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPFLQHVDAKVSGLRSLTTLRALGAKQKALS 120
 QY 121 PPDAASAAPLRITTTADTFRKLFVYNSFNLRGKLUYTGACRTGD 165

Db 121 PPDAASAAPLRITTTADTFRKLFVYNSFNLRGKLUYTGACRTGD 165
 RESULT 9
 ABB77896
 ID ABB77896 standard; protein; 165 AA.
 XX
 AC ABB77896;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Homo sapiens.
 XX
 FN WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EP014434.
 XX
 PR 20-DEC-2000; 2000EP-00127891.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 PI Wozny M;
 XX
 DR WPI; 2002-566640/60.
 XX
 FT Novel conjugate of erythropoietin glycoprotein with polyethylene glycol,
 PT useful for treating diseases correlated with anaemia in chronic renal
 PT failure patients and acquired immunodeficiency syndrome.
 XX
 PS Claim 26; Fig 1; 40pp; English.
 XX
 CC The present sequence represents a human erythropoietin (EPO) protein. It
 CC was used to produce conjugates of the invention. The specification
 CC describes a conjugate comprising an EPO glycoprotein having an N-terminal
 CC alpha-amino group, chosen from human EPO (hEPO) or its analogues (where
 CC hEPO is modified by addition of 1-6 glycosylation sites or a
 CC rearrangement of a glycosylation site). The glycoprotein is covalently
 CC linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo
 CC biological activity of causing bone marrow cells to increase production
 CC of reticulocytes and red blood cells. The conjugate increased circulating
 CC half-life and plasma residence time, decreased clearance, increased
 CC clinical activity in vivo, improved potency and stability, when compared
 CC to unmodified EPO. The EPO conjugate is useful for preparing medicaments
 CC for the treatment and prophylaxis of diseases correlated with anaemia in
 CC chronic renal failure patients (CRF), acquired immunodeficiency syndrome
 CC (AIDS) and for treating cancer patients undergoing chemotherapy. It is
 CC also useful for treating patients by stimulating the division and
 CC differentiation of committed erythroid progenitors in the bone marrow

ABB83621
ID ABB83621 standard; protein; 165 AA.
XX
AC ABB83621;
XX
DT 10-OCT-2002 (first entry)
XX
DE Protein #1 relating to modified erythropoietin glycoprotein.
XX
KW Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
KW cancer.
XX
OS Unidentified.
XX
PN NO200003372-A.
XX
PD 03-JAN-2001.
XX
PF 28-JUN-2000; 2000NO-00003372.
XX
PR 02-JUL-1999; 99US-0142254P.
PR 23-AUG-1999; 99US-0150225P.
PR 31-AUG-1999; 99US-0151548P.
PR 17-NOV-1999; 99US-0166151P.
XX
FA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
FI Bailon PS;
XX
DR WPI; 2001-135308/14.
XX
PT New conjugate having modified erythropoietin glycoprotein useful for
PT stimulating red blood cell production and for treating diseases
PT correlated with anaemia in chronic renal failure, AIDS or cancer patients.
XX
PS Disclosure; Page 21-22; 30pp; Norwegian.
XX
CC This invention relates to new conjugate having a modified erythropoietin
CC glycoprotein, useful for stimulating red blood cell production, and for
CC treating or preventing diseases correlated with anaemia in chronic renal
CC failure, AIDS or cancer patients. The present sequence is a protein
CC related to the invention
XX
SQ Sequence 165 AA;
Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
RESULT 7
AAB66697
ID AAB66697 standard; protein; 165 AA.
XX
AC AAB66697;
XX
DT 06-APR-2001 (first entry)
XX
DE Human erythropoietin protein #1.
XX
KW Erythropoietin; EPO; reticulocytes; red blood cell; ethylene glycol;

XX
XX chronic renal failure; AIDS; cancer.
OS Homo sapiens.
XX
PN WO200102017-A2.
XX
PD 11-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-EP006009.
XX
PR 02-JUL-1999; 99US-0142243P.
PR 05-AUG-1999; 99US-0147452P.
PR 30-AUG-1999; 99US-0151454P.
XX
FA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
FI Burg J, Hilger B, Josel H;
XX
DR WPI; 2001-147051/15.
XX
PT Novel erythropoietin-glycoprotein conjugate useful for treating diseases
PT correlated with anaemia in chronic renal failure patients, AIDS and for
PT treating cancer, is linked to polyethylene glycol through linker.
XX
PS Claim 19; Fig 1; 40pp; English.
XX
CC The present invention relates to a conjugate comprising, human
CC erythropoietin glycoprotein (GPO) having at least one free amino group
CC and having in vivo biological activity of causing an increase the
CC production of reticulocytes and red blood cells, covalently linked to 1-3
CC lower-alkoxy poly(ethylene glycol) groups through a linker. The invention
CC is useful for preparation of medicaments for the treatment of prophylaxis
CC of disease correlated with anaemia in chronic renal failure patients
CC (CRF), AIDS and for the treatment of cancer patients undergoing
CC chemotherapy
XX
SQ Sequence 165 AA;
Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTLTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKLFVYSNFRGLKLYTGEACRTGD 165
RESULT 8
AAM53061
ID AAM53061 standard; protein; 165 AA.
XX
AC AAM53061;
XX
DT 25-MAR-2002 (first entry)
XX
DE Human erythropoietin (hEPO), 165 residue form.
XX
KW Human; erythropoietin; EPO; hEPO; haemostatic; red blood cell;
KW blood disorder; anaemia; chronic renal failure; CRF; AIDS;
KW acquired immunodeficiency syndrome; cancer chemotherapy; haemostatic;
KW anti-HIV; antianaemic.
XX
OS Homo sapiens.
XX
FA Key Location/Qualifiers
XX
FH

QY 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165
 DB 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165

RESULT 4

AA99705
 ID AAY99705 standard; protein; 165 AA.

AC AAY99705;

DT 15-SEP-2000 (first entry)

XX Non-glycosylated erythropoietin analogue NGE-166delta.

KW Human; non-glycosylated erythropoietin analogue; NGEA; haematocrit;
 KW antianemic; anaemia; erythropoiesis promoter; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO200032772-A2.

PN 08-JUN-2000.

XX 23-NOV-1999; 99WO-US027801.

XX 30-NOV-1998; 98US-0110289P.

XX (ELIL) LILLY & CO ELT.

PI Beals JM, Glaesner W, Micanovic R, Millican RL, Witcher DR;

XX WPI; 2000-412320/35.

DR N-PSDB; AAA48373.

XX Non-glycosylated erythropoietic compound useful for increasing hematocrit
 PT level in mammal with insufficient hematocrit levels in conditions such as
 PT anemia, comprises protein covalently bonded to polymer.

XX Claim 2; Page 93-94; 94pp; English.

XX The present sequence is a non-glycosylated erythropoietin analogue (NGEA)
 CC designated NGE-166delta. The protein sequence is identical to the
 CC sequence of wild-type human non-glycosylated erythropoietin NGE except
 CC that Arg at position 166 is deleted. NGE promotes erythropoiesis and can
 CC therefore be used to increase haematocrit levels in mammals with
 CC conditions such as anaemia, in which levels of haematocrit are
 CC insufficient. NGE analogues can also be used to treat such conditions.
 CC NGEAs do not themselves cause a significant increase in haematocrit but
 CC they acquire that property once they are derivatised with polyethylene
 CC glycol polymers. The analogues can be produced using a linkerless
 CC aldehyde modification process. They show stability and bioactivity in
 CC vivo. The nucleotide sequence encoding this protein was constructed
 CC synthetically by in vitro hybridisation using a set of six overlapping
 CC oligonucleotides from the positive strand of human erythropoietin cDNA
 CC with six complementary oligonucleotides (negative strand). The codon
 CC usage was 100% optimised for E. coli codon usage. The hybridised
 CC oligonucleotides were ligated with T4 DNA ligase and the ligation product
 CC amplified by PCR. The nucleotide sequence was used to express the protein
 CC in host cells

XX Sequence 165 AA;

Query Match 100.0%; Score 846; DB 3; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLCDRSVRLRYLLEAKEAENITTCGAHCNSLNENITVPDVKVFNKRMVEVGQQA 60
 DB 1 APRRLCDRSVRLRYLLEAKEAENITTCGAHCNSLNENITVPDVKVFNKRMVEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQFWPEPLQHVVDKAVSGLSRLTLRALGAQKEAITS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQFWPEPLQHVVDKAVSGLSRLTLRALGAQKEAITS 120
 QY 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165
 DB 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165

RESULT 5

AA84525

ID AAB84525 standard; protein; 165 AA.

XX AAB84525;

DT 05-SEP-2001 (first entry)

XX Amino acid sequence of human erythropoietin (EPO) protein.

XX Erythropoietin; EPO; erythropoietin stimulating protein; NESP;
 KW sustained release.

XX Homo sapiens.

XX WO200130320-A1.

XX 03-MAY-2001.

XX 23-OCT-2000; 2000WO-US029257.

XX 22-OCT-1999; 99US-00426566.

XX 13-OCT-2000; 2000US-00687981.

XX (AMGE-) AMGEN INC.

XX Burke P, Klumb L, Murphy K, Herberger J, French DL;

XX WPI; 2001-417552/44.

XX Sustained release composition comprises an active biological ingredient,
 PT notably a protein or other biopolymer, particularly erythropoietin
 PT stimulating protein, in biocompatible, biodegradable polymeric
 PT microparticles.

XX Disclosure; Page 56; 61pp; English.

XX The present sequence encodes a human erythropoietin (EPO) protein. The
 CC specification describes a composition for the sustained release of
 CC biologically active EPO stimulating protein (NESP). The reduced frequency
 CC of administration of NESP, which requires preferably injection by skilled
 CC personnel, improves patient compliance. Also, sustained release reduces
 CC the nature and severity of any side effects of the drug

XX Sequence 165 AA;

Query Match 100.0%; Score 846; DB 4; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.8e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLCDRSVRLRYLLEAKEAENITTCGAHCNSLNENITVPDVKVFNKRMVEVGQQA 60
 DB 1 APRRLCDRSVRLRYLLEAKEAENITTCGAHCNSLNENITVPDVKVFNKRMVEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQFWPEPLQHVVDKAVSGLSRLTLRALGAQKEAITS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQFWPEPLQHVVDKAVSGLSRLTLRALGAQKEAITS 120

QY 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165

DB 121 PDAAASAPLRTITADTFKFLFRVYSNFRGKLGKLYTGEACRTGD 165

RESULT 6


```
Db 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKNFYAKRMEVGQQA 60
61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
Qy 121 PPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
Db 121 PPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165

RESULT 2
AAB03760
ID AAB03760 standard; protein; 165 AA.
AC AAB03760;
XX
XX 04-OCT-2000 (first entry)
DT Human erythropoietin (EPO) amino acid sequence.
DE Erythropoietin; EPO; human; erythroblast differentiation; anaemia;
XX large scale production; renal failure.
KW Homo sapiens.
XX
XX WO200027997-A1.
XX 18-MAY-2000.
XX
XX 08-NOV-1999; 99WO-US026240.
XX
XX 06-NOV-1998; 98AR-00105611.
XX 23-FEB-1999; 99AR-00100681.
XX
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376519/32.
XX
XX A novel method for the massive culture of recombinant mammalian cells
XX producing recombinant human erythropoietin.
XX Example 8; Page 11-12; 23pp; English.
XX
XX This sequence represents the human erythropoietin amino acid sequence.
XX Erythropoietin is a glycoprotein that stimulates erythroblast
XX differentiation in the bone marrow. The present invention relates to a
XX method for the large scale production of human EPO from recombinant
XX mammalian cells. The method comprises culturing mammalian cells which
XX express recombinant human EPO in culture medium comprising insulin.
XX Erythropoietin can be used to treat anaemia derived from renal failure.
XX The method allows for the industrial scale production of EPO, and
XX overcomes the problems of low reproducibility and output quality which
XX are encountered with previous production methods
XX
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
Qy 121 PPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165
```

```
Db 121 PPDAASAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGD 165

RESULT 3
AAY94605
ID AAY94605 standard; protein; 165 AA.
XX
XX AAY94605;
XX
XX 28-NOV-2000 (first entry)
DT Human erythropoietin.
DE Human; erythropoietin; EPO; purification; anaemia.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 24 /note= "N-Glycosylation site"
FT Modified-site 38 /note= "N-Glycosylation site"
FT Modified-site 83 /note= "N-Glycosylation site"
FT Modified-site 126 /note= "N-Glycosylation site"
FT Modified-site /note= "O-Glycosylation site"
XX
XX WO200027869-A1.
XX
XX 18-MAY-2000.
XX
XX 08-NOV-1999; 99WO-US026241.
XX
XX 06-NOV-1998; 98AR-00105610.
XX 23-FEB-1999; 99AR-00100680.
XX
XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.
XX
XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX WPI; 2000-376485/32.
XX
XX Novel methods for purifying recombinant human erythropoietin from
XX mammalian cell culture reagents.
XX Claim 16; Page 18; 30pp; English.
XX
XX The present invention relates to a method for purifying erythropoietin
XX (EPO) for treatment of disease, especially anaemia. The method involves
XX treating cell culture supernatants with differential precipitation,
XX hydrophobic interaction chromatography, diafiltration, anionic and
XX cationic exchange chromatography and molecular exclusion chromatography.
XX The present sequence is the protein from the culture supernatant of
XX transfected cell lines, after purification by the above process. The
XX sequence shows total homology with natural human EPO. The advantage of
XX this method is that high purity and quality EPO is produced. A further
XX advantage is that the process does not involve the use of organic
XX solvents that may harm the environment
XX
XX Sequence 165 AA;
SQ
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKAEENITTCABHCSLNENITVPDTKNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKQKAIS 120
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:06:32 ; Search time 62.3112 Seconds
(without alignments)
949.915 Million cell updates/sec

Title: US-10-780-297-1
Perfect score: 846
Sequence: 1 APPRLICDSRVLEAK.....SNFLGKLYTGACRTGD 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesecp 23Sep04: *
1: Genesecp1980s: *
2: Genesecp1990s: *
3: Genesecp2000s: *
4: Genesecp2001s: *
5: Genesecp2002s: *
6: Genesecp2003as: *
7: Genesecp2003bs: *
8: Genesecp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	3	AAY93445 Amino aci
2	846	100.0	165	3	AAB03760 Human ery
3	846	100.0	165	3	AAY94605 Human ery
4	846	100.0	165	3	AAY99705 Non-glyco
5	846	100.0	165	4	AAB84525 Amino aci
6	846	100.0	165	4	AAB83621 Protein #
7	846	100.0	165	4	AAB66697 Human ery
8	846	100.0	165	5	AAM53061 Human ery
9	846	100.0	165	5	ABBT7896 Amino aci
10	846	100.0	165	6	ABP98492 Human ery
11	846	100.0	165	8	ADL06780 Human 165
12	846	100.0	165	8	ADN49745 Mature hu
13	846	100.0	165	8	ADN49745 Mature hu
14	846	100.0	165	8	ADN49745 Mature hu
15	846	100.0	166	1	AAP70398 Sequence
16	846	100.0	166	2	AAR23593 Recombina
17	846	100.0	166	2	AAM58404 Human ery
18	846	100.0	166	2	AAM58404 Human ery
19	846	100.0	166	2	AAM58404 Human ery
20	846	100.0	166	3	ABT07030 Modified
21	846	100.0	166	4	ABE83622 Protein #
22	846	100.0	166	4	AAB02641 Human ery
23	846	100.0	166	4	AAB66698 Human ery
24	846	100.0	166	5	ABG92101 Human ery
25	846	100.0	166	5	AAM53062 Human ery
					Abb77897 Amino aci

26	846	100.0	166	5	ADG65661 Human ery
27	846	100.0	166	6	ABR39996 Human ery
28	846	100.0	166	6	ABR57500 Human ery
29	846	100.0	166	7	ADP70839 Human ery
30	846	100.0	166	8	ADL92150 Erythro
31	846	100.0	166	8	ADK70564 Human ery
32	846	100.0	166	8	ADL88867 Human ery
33	846	100.0	166	8	ADL06781 Human 166
34	846	100.0	166	8	ADN59416 Human 166
35	846	100.0	167	1	AAP50299 Human rec
36	846	100.0	167	1	AAP50298 Human rec
37	846	100.0	169	5	ABB77899 Amino aci
38	846	100.0	174	5	ABB77898 Amino aci
39	846	100.0	174	5	ABB77900 Amino aci
40	846	100.0	188	1	AAP60599 Clone lam
41	846	100.0	188	1	AAP61195 Erythro
42	846	100.0	192	7	ADP16588 Human alb
43	846	100.0	192	7	ADP16589 Human alb
44	846	100.0	192	7	ADP15305 Human alb
45	846	100.0	192	7	ADP16727 Human alb

ALIGNMENTS

RESULT 1
AAY93445
ID AAY93445 standard; protein; 165 AA.
XX
AC AAY93445;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of human erythropoietin.
XX
KW Human; erythropoietin; EPO; anaemia; renal failure.
XX
OS Homo sapiens.
XX
PN WO200028066-A1.
XX
PD 18-MAY-2000.
XX
PF 08-NOV-1999; 99WO-US026238.
XX
PR 06-NOV-1998; 98AR-00105609.
XX
PR 23-FEB-1999; 99AR-00100679.
XX
PA (STER-) STERRENELD BIOTECHNOLOGIE NORTH AMERICA.
XX
PI Carcagno CM, Criscuolo M, Melo C, Vidal JA;
XX
DR WPI; 2000-376574/32.
XX
PT New host cell producing recombinant human erythropoietin (EPO) used for
PT large scale production of EPO.
XX
PS Claim 1; Page 26-27; 51pp; English.
XX
CC The present sequence represents human erythropoietin protein. The
CC specification describes a host cell line which is used to produce human
CC erythropoietin (EPO). EPO is a glycoprotein. The cell line is used for
CC the production of recombinant human erythropoietin. The protein is used
CC for the treatment of anaemia, especially anaemia derived from renal
XX failure
XX
SQ Sequence 165 AA;
Query Match 100.0%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred.No. 1.8e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APPRLICDSRVLEAKENITTCGAHCSLNENITVPDTKVNFWAKMEVGGQA 60

RP SEQUENCE OF 28-193, AND DISULFIDE BONDS.
RC TISSUE=Urine;
RX MEDLINE=8614080; PubMed=3949763;
RA Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
RT "Structural characterization of human erythropoietin.";
RL J. Biol. Chem. 261:3116-3121(1986).
RN [7]
RP PRELIMINARY SEQUENCE OF 28-57.
RX MEDLINE=84135751; PubMed=669899;
RA Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
RA Goto M.;
RT "Isolation of human erythropoietin with monoclonal antibodies.";
RL J. Biol. Chem. 259:2707-2710(1984).
RN [8]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=88153657; PubMed=3346214;
RA Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
RA Kobata A.;
RT "Comparative study of the asparagine-linked sugar chains of human
erythropoietins purified from urine and the culture medium of
recombinant Chinese hamster ovary cells.";
RL J. Biol. Chem. 263:3657-3663(1988).
RN [9]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=89118279; PubMed=3219367;
RA Sasaki H., Ochi N., Dell A., Fukuda M.;
RT "Site-specific glycosylation of human recombinant erythropoietin:
analysis of glycopeptides or peptides at each glycosylation site by
fast atom bombardment mass spectrometry.";
RL Biochemistry 27:8618-8626(1988).
RN [10]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=92314463; PubMed=1820196;
RA Takeuchi M., Kobata A.;
RT "Structures and functional roles of the sugar chains of human
erythropoietins.";
RL Glycobiology 1:337-346(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
RA Syed R.S., Reid S.W., Li C., Cheatham J.C., Aoki K.H., Liu B.,
RA Zhan H., Oslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
RA Elliott S., Siney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
critically on receptor orientation.";
RL Nature 385:511-516(1998).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
CC -!- PHARMACEUTICAL: Used for the treatment of anemia. Available under
the names Epogen (Amgen), Epogin (Chugai), Epomax (Eli Lilly), Eprex
(Janssen-Cilag), NeoRecormon or Recormon (Roche), and Procrit
(Ortho Biotech). Variations in the glycosylation pattern of EPO
distinguishes these products. Epogen, Epogin, Eprex and Procrit
are generically known as epoetin alfa, NeoRecormon and Recormon as
epoetin beta and Epomax as epoetin omega.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC -!- DATABASE: NAME=R&D Systems' cytokine source book: EPO;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/))
or send an email to license@isb-sib.ch)
CC -----
EMBL; X02159; CAA26095.1; -

DR EMBL; X02157; CAA26094.1; -
DR EMBL; M11319; AAA52400.1; -
DR EMBL; AF053356; AAC78791.1; -
DR EMBL; AF023308; AAF23132.1; -
DR EMBL; AF023306; AAF23132.1; JOINED.
DR EMBL; AF023307; AAF23132.1; JOINED.
DR EMBL; AF023310; AAF23133.1; -
DR EMBL; AF023309; AAF23133.1; JOINED.
DR EMBL; AF023311; AAF17572.1; -
DR EMBL; AF023314; AAF23134.1; -
DR EMBL; AF023312; AAF23134.1; JOINED.
DR EMBL; AF023313; AAF23134.1; JOINED.
DR EMBL; S65458; AAD13964.1; -
DR PIR; A01855; ZUHU.
DR PDB; 1BUY; NMR; A=28-193.
DR PDB; 1CN4; X-ray; C=28-193.
DR PDB; 1EER; X-ray; A=28-193.
DR GlycoSuiteDB; P01588; -
DR Gene; HGNC:3415; EPO.
DR MIM; 133170; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006950; P:response to stress; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythropo.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PROSITE; PRO0272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
KW Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 27
FT CHAIN 28 193 Erythropoietin.
FT PROPEP 190 193 Removed in mature form (Probable).
FT DISULFID 34 188
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65 N-linked (GlcNAc...).
FT CARBOHYD 110 110 /FTid=CAR_000052.
FT CARBOHYD 153 153 N-linked (GlcNAc...).
FT CARBOHYD 131 132 /FTid=CAR_000166.
FT VARIANT 149 149 N-linked (GlcNAc...).
FT VARIANT 40 40 /FTid=CAR_000192.
FT CONFLICT 85 85 O-linked (GalNAc...).
FT CONFLICT 140 140 SL -> NF (in an hepatocellular
carcinoma)
FT CONFLICT 32 34 /FTid=VAR_009870.
FT CONFLICT 36 52 P -> Q (in an hepatocellular carcinoma).
FT CONFLICT 53 55 /FTid=VAR_009871.
FT TURN 57 58 E -> Q (in Ref. 1; CAA26095).
FT STRAND 61 68 Q -> QQ (in Ref. 5).
FT STRAND 73 73 G -> R (in Ref. 1; CAA26095).
FT HELIX 75 78
FT TURN 79 80
FT HELIX 83 109
FT HELIX 118 138
FT TURN 139 140
FT HELIX 141 147
FT TURN 148 149
FT STRAND 160 164
FT HELIX 165 177
FT TURN 178 178
FT HELIX 179 188
SQ SEQUENCE 193 AA; 21306 MW; C91F0B4C26A52033 CRC64;
Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.4e-72;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:06:58 ; Search time 120.634 Seconds
(without alignments)
786.979 Million cell updates/sec

Title: US-10-780-297-1

Perfect score: 846

Sequence: 1 APRRLCDRLVRLLEAK.....SNFLRGLKLYTGACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	193	1	EPO_HUMAN
2	846	100.0	193	2	Asp22357
3	764.5	90.4	192	1	EPO_MACFA
4	759.5	89.8	192	1	EPO_MACMU
5	723	85.5	192	2	Q867B1
6	706	83.5	192	1	EPO_FELCA
7	701	82.9	192	1	EPO_RAT
8	693	81.9	206	2	Q6FWU5
9	692.5	81.9	206	2	As77874
10	689	81.4	192	1	EPO_BOVIN
11	689	81.4	192	1	EPO_MOUSE
12	685.5	80.4	194	1	EPO_SHEEP
13	680.5	80.4	195	2	Q8K22
14	680.5	80.4	195	2	Q8K33
15	678	80.1	192	1	EPO_PIG
16	678	80.1	192	2	Q8H89
17	678	80.1	192	2	Q8H89
18	678	80.1	192	2	Q8H81
19	678	80.1	194	2	Q8H82
20	674	79.7	192	2	Q8H82
21	663	78.4	133	2	Q8H28
22	658	77.8	133	2	Q8H28
23	638	75.4	175	1	EPO_CANFA
24	627	74.1	131	2	Q8H28
25	607	71.7	133	2	Q8H28
26	554	65.5	133	2	Q8H28
27	241	28.5	195	2	Q8UAM1
28	241	28.5	195	2	Q8UAM1
29	238	28.1	182	2	Q8J23
30	238	28.1	182	2	Q8J23
31	238	28.1	185	2	Q8J22

RESULT 1

ID	EPO_HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.			
RT	"Isolation and characterization of the human erythropoietin gene."			
RT	erythropoietin."			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene."			
RT	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=9799793;			
RA	Gloekner G., Scherer S., Schattevov R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes."			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	Rupert J.L., Hochachka P.W.;			
RT	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population."			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-ASN-PHS-132 AND GLN-149.			
RP	MEDLINE=9384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma."			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

ALIGNMENTS

32	238	28.1	185	2	AAQ72467
33	188	22.2	50	2	Q9QV40
34	113	13.4	177	2	Q6IVE9
35	109	12.9	352	1	TPO_CANFA
36	89	10.5	353	1	TPO_HUMAN
37	88	10.4	323	2	Q8ZDC8
38	88	10.4	323	2	AAS62651
39	87.5	10.3	346	2	Q8Z2M5
40	87.5	10.3	346	2	Q8ZKZ4
41	87.5	10.3	432	2	Q7QDZ2
42	85	10.0	3722	2	P94873
43	83	9.8	256	2	Q8ZAY4
44	83	9.8	236	2	AAS64044
45	83	9.8	301	2	Q7PKU0

AAQ72467 fugu rubr
Q9QV40 rattus sp.
Q6IVE9 gallus gall
P42705 canis faml
P40225 homo sapien
Q8ZDC8 yersinia pe
AAS62651 yersinia
Q8Z2M5 salmonella
Q8ZKZ4 salmonella
Q7QDZ2 anopheles g
P94873 lysobacter
Q8ZAY4 yersinia pe
AAS64044 yersinia
Q7PKU0 anopheles g

Query Match	80.1%;	Score 678;	DB 1;	Length 190;
Best Local Similarity	82.0%;	Pred. M. 2.3e-56;		
Matches 137;	Conservative	7;	Mismatches 21;	Indels
Qy	1	APPLICDSRVLERVLLLEAKEAEENITTCACRHCLSNENITVPDTKVNFYFA		
Db	23	APPLICDSRVLERIYIILEAKEGENATWGCACSCSFSENIITVPDTKVNFYA		
Qy	61	VEVWQGLIALLSAEVLRGQALLVNSSQWPEIQLQHVDRKAVSGLRISLTLLIR		
Db	83	MEVWQGLIALLSSEALIQGQALLANSQSSEALQLHVDKAVSGLRISLTSLIR		
Qy	121	PPDA--ASAAPLRITITADTFKLFPRVYSNFIURGKLKLYTGACRTGD 16		
Db	143	LPDAPSSASPLRIFAVDTLCKLFNTSNFIURGKLKLYTGACRRRD 18		

Search completed: December 3, 2004, 13:38:12
Job time : 122.634 secs

```

RESULT 15
EPO_PIG
ID -EPO_PIG
AC P49157;
STANDARD; PRT; 190 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN Name=EPO;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
RN
RC SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993)
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L10607; AAA31029.1; -.
DR PIR; I46578; I46578.
DR HSSP; P01588; 1CN4.
DR InterPro; IPRO09079; 4 helix cytokine.
DR InterPro; IPRO01323; EPO_TPO.
DR InterPro; IPRO03013; Erythroptn.
DR Pfam; PF00758; EPO_TPO.1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
KW NON TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 190 Erythropoietin.
FT DISULFD 29 185 By similarity.
FT DISULFD 51 55 By similarity.
FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 190 AA; 20888 MW; A75BDDCCS5077E2A CRC64;

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:06:32 ; Search time 62.6888 Seconds
(without alignments)
949.915 Million cell updates/sec

Title: US-10-780-297-2

Perfect score: 851

Sequence: 1 APRLICDSRVLYRLEAK.....NPLRGKLYTGCACTGDR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep23Sep04:*

1: genesep1980s:*

2: genesep1980s:*

3: genesep2000s:*

4: genesep2000s:*

5: genesep2002s:*

6: genesep2003as:*

7: genesep2003bs:*

8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	166	1 AAP70398	Aap70398 Sequence
2	851	100.0	166	2 AAR23593	Aar23593 Recombina
3	851	100.0	166	2 AAW58404	Aaw58404 Human ery
4	851	100.0	166	2 AAW77780	Aaw77780 Human EPO
5	851	100.0	166	3 ABB07030	Abb07030 Modified
6	851	100.0	166	4 ABB3622	Abb3622 Protein #
7	851	100.0	166	4 AAE02641	Aae02641 Human ery
8	851	100.0	166	4 AAB66698	Aab66698 Human ery
9	851	100.0	166	5 ABG92101	Abg92101 Human ery
10	851	100.0	166	5 AAM53062	Aam53062 Human ery
11	851	100.0	166	5 ABB77897	Abb77897 Amino aci
12	851	100.0	166	5 ADG56661	Adg56661 Human ery
13	851	100.0	166	6 ABR39996	Abr39996 Human ery
14	851	100.0	166	6 ABR57500	Abr57500 Human ery
15	851	100.0	166	7 ADF70839	Adf70839 Human ery
16	851	100.0	166	8 ADL92150	Adl92150 Erythro
17	851	100.0	166	8 ADK70564	Adk70564 Human ery
18	851	100.0	166	8 ADL88867	Adl88867 Human ery
19	851	100.0	166	8 ADL06781	Adl06781 Human 166
20	851	100.0	166	8 ADO59416	Ado59416 Human 166
21	851	100.0	167	1 AAP50299	Aap50299 Human rec
22	851	100.0	167	1 AAP50298	Aap50298 Human rec
23	851	100.0	169	5 ABB77899	Abb77899 Amino aci
24	851	100.0	174	5 ABB77898	Abb77898 Amino aci
25	851	100.0	174	5 ABB77900	Abb77900 Amino aci

ALIGNMENTS

RESULT 1

AAP70398

ID AAP70398 standard; protein; 166 AA.

XX

AC AAP70398;

XX

DT 19-FEB-1991 (first entry)

XX

DE Sequence of human erythropoietin (EPO).

XX

XX Mega-karyocyte-platelet growth factor; hormone;

KW mega-karyocyte colony stimulating factor; therapy;

KW small acetyl cholinesterase positive cell; erythrocyte growth effect.

XX

OS Homo sapiens.

XX

PN JP62149624-A.

XX

PD 03-JUL-1987.

XX

PF 15-AUG-1986; 86JP-00191542.

XX

PR 13-SEP-1985; 85JP-00203049.

XX

(KAWA/) KAWAKITA M.

XX

WPI; 1987-224837/32.

XX

Megakaryocyte-platelet growth factor - contains as active component human erythropoietin and is used to treat diseases caused by decrease in platelets.

PT

PS Disclosure; Page 181; app; Japanese.

XX

CC All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-platelet growth factor contains human EPO as an active principle. Human EPO has a megakaryocyte colony-stimulating activity and increases the ratio of small acetyl cholinesterase positive cell (SACHE+) which is immature megakaryocyte. Human EPO effects megakaryocyte-platelet system other than an erythrocyte growth effect. Megakaryocyte-platelet growth is usable as a remedy for diseases caused by a platelet decrease

XX

SQ Sequence 166 AA;

XX

Query Match

Best Local Similarity 100.0%;

Matches 166; Conservative 100.0%;

Mismatches 0;

Indels 0;

Gaps 0;

Length 166;

Pred. No. 7.4e-87;

QY 1 APRRLICDSRVLEKYLEAKENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 DB 1 APRRLICDSRVLEKYLEAKENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFRKLFRVYNFLRGKLYTGEACRTGDR 166
 DB 121 PPDAASAAPLRTITADTFRKLFRVYNFLRGKLYTGEACRTGDR 166

RESULT 2
 AAR23593
 ID AAR23593 standard; protein; 166 AA.
 AC AAR23593;
 XX 20-OCT-1992 (first entry)
 DT Recombinant hematopoietic molecule portion 2.
 DE Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis.
 KW Homo sapiens.
 OS WO9206116-A.
 FN 16-APR-1992.
 PD 26-SEP-1991; 91WO-US007053.
 PF 28-SEP-1990; 90US-00589958.
 PR (ORTH) ORTHO PHARM CORP.
 PA Rosen JI;
 PI WPI; 1992-150819/18.
 DR Recombinant haematopoietic molecules useful in treating anaemia(s) -
 PT comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and
 later myeloid differentiation activity.
 PS Disclosure; Page 32; 82pp; English.

CC This protein sequence given comprises the entire amino acid sequence of
 CC human erythropoietin (EPO). EPO leads to the maturation of erythrocytes
 CC and is therefore designated as a late myeloid differentiation factor
 CC (MDF). Within the scope of the invention hybrid molecules were produced
 CC which contain at least a portion of an early MDF and at least a portion
 CC of a late MDF covalently linked. The EPO sequence given is effective
 CC within the scope of the invention in full or in a truncated version.
 CC Amino acids 7-161 act as a late MDF when recombined with an early MDF eg.
 CC IL-3. These compounds can be used to promote haematopoiesis in a patient.
 CC The bonding of the early and late factors allows a very high conc. of
 CC late MDF at the surface of a cell which the early MDF is bound. It also
 CC allows the early MDA to act more specifically to stimulate only the
 CC desired lineage, thus reducing undesirable effects. These compounds are
 CC useful for treating anaemias of various origins eg. renal failure and
 CC AIDS. It is easier to produce and administer one recombinant molecule
 CC rather than two separate molecules
 CC Sequence 166 AA;

Query Match 100.0%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLEKYLEAKENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 DB 1 APRRLICDSRVLEKYLEAKENITTCAGHCSLNENITVPDTKKNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQFWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFRKLFRVYNFLRGKLYTGEACRTGDR 166
 DB 121 PPDAASAAPLRTITADTFRKLFRVYNFLRGKLYTGEACRTGDR 166

RESULT 3
 AAW58404
 ID AAW58404 standard; protein; 166 AA.
 AC AAW58404;
 XX 12-OCT-1998 (first entry)
 DT Human erythropoietin.
 DE Erythropoietin receptor agonist; EPO; human; anaemia;
 KW haematopoietic deficiency; red blood cell; erythroid progenitor;
 KW bone marrow suppression.
 OS Homo sapiens.
 XX WO9818926-A1.
 FN 07-MAY-1998.
 PD 23-OCT-1997; 97WO-US018703.
 PF 25-OCT-1996; 96US-0034044P.
 PR (SEAR) SEARLE & CO G D.
 PA McWherter CA, Feng Y, Summers N;
 PI WPI; 1998-272221/24.
 DR N-PSDB; AAV31031.
 XX Human erythropoietin receptor agonist polypeptide - used to stimulate the
 PT production of red blood cells in a patient.
 PS Claim 1; Page 93; 112pp; English.

CC A claimed human erythropoietin (EPO) receptor agonist polypeptide
 CC comprises a modified EPO amino acid sequence given in AAW58404, where (a)
 CC optionally 1-6 amino acids from the N-terminus and 1-5 from the C-
 CC terminus can be deleted, (b) the N-terminus is joined to the C-terminus
 CC directly or through a linker (see AAW58405-12) capable of joining the N-
 CC terminus to the C-terminus, (c) there are new C- and N-termini at any two
 CC consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42,
 CC 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-
 CC 109 to 131-132, and (d) optionally the agonist polypeptide is preceded by
 CC Met, Ala, or Met-Ala. 60 Of these circularly permuted EPO receptor
 CC agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid
 CC molecules (see AAV30971-V31030) encoding novel EPO receptor agonists; a
 CC method of producing an EPO receptor agonist using transformed or
 CC transfectected host cells; and methods for stimulating the production of
 CC haematopoietic cells, for selective ex vivo expansion of erythroid
 CC progenitors, and treating patients having a haematopoietic disorder using
 CC the EPO receptor agonists. The EPO receptor agonists retain one or more
 CC activities of native EPO and may also show improved haematopoietic cell-
 CC stimulating activity and/or an improved activity profile which may
 CC include reduction of undesirable biological activities associated with
 CC native EPO and/or have improved physical properties such as increased
 CC solubility, stability and refold efficiency
 CC Sequence 166 AA;

Query Match 100.0%; Score 851; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;


```
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSVLEKYLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 60
DQ 1 APPRLICDSVLEKYLEAKAEENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 60
QY 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSLRSLITLLRALGQAEKIS 120
DQ 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSLRSLITLLRALGQAEKIS 120
QY 121 PPDAASAPLRTITADTFKRLFRVYSNPLRGKLYTGECACRTGDR 166
DQ 121 PPDAASAPLRTITADTFKRLFRVYSNPLRGKLYTGECACRTGDR 166

RESULT 4
AAW77780
ID AAW77780 standard; protein; 166 AA.
AC AAW77780;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human EPO receptor agonist polypeptide.
XX
KW Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO;
KW human; chimeric protein; stem cell expansion; tumour; infection;
KW autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
XX
OS Homo sapiens.
XX
PH Key
FT Misc-difference 1. .6
FT /note= "1-6 amino acids of the N-terminus are optionally
FT deleted"
FT Misc-difference 23. .24
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 24. .25
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 25. .26
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 26. .27
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 27. .28
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 28. .29
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 29. .30
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 30. .31
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 31. .32
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 32. .33
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 33. .34
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 34. .35
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 35. .36
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 36. .37
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 37. .38
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 38. .39
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 39. .40
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 40. .41
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 41. .42
FT /note= "possible positions of new C- and N-termini"
FT
FT Misc-difference 42. .43
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 43. .44
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 44. .45
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 45. .46
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 46. .47
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 47. .48
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 48. .49
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 49. .50
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 50. .51
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 51. .52
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 52. .53
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 53. .54
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 54. .55
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 55. .56
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 56. .57
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 57. .58
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 77. .78
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 78. .79
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 79. .80
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 81. .82
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 82. .83
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 84. .85
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 85. .86
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 86. .87
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 87. .88
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 88. .89
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 108. .109
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 109. .110
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 110. .111
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 111. .112
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 112. .113
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 113. .114
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 114. .115
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 115. .116
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 116. .117
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 117. .118
FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 118. .119
FT /note= "possible positions of new C- and N-termini"
```

FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 119..120
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 120..121
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 121..122
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 122..123
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 123..124
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 124..125
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 125..126
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 126..127
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 127..128
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 128..129
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 129..130
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 130..131
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 131..132
 FT /note= "possible positions of new C- and N-termini"
 FT Misc-difference 132..133
 FT /note= "1-5 amino acids of the C-terminus are optionally deleted"
 FT
 PN WO9817810-A2.
 XX
 XX 30-APR-1998.
 XX
 XX 23-OCT-1997; 97WO-US020037.
 XX
 XX 25-OCT-1996; 96US-0029629P.
 XX
 XX (SEAR) SEARLE & CO G D.
 XX
 XX McWherter CA, Feng Y, McKearn JP, Summers NL, Staten NR;
 PI Streeter PR, Minnerly JC, Minster NI, Woulfe SL;
 XX
 XX WPI; 1998-261504/23.
 XX
 XX Multi-functional chimeric haematopoietic receptor agonist - useful to
 FT treat haematopoietic disorders, tumours, infections or autoimmune
 FT diseases.
 FT
 PS Claim 1; Page 762; 841pp; English.
 XX
 CC A human erythropoietin (EPO) receptor agonist polypeptide comprises a
 CC modified EPO amino acid sequence of the formula provided in AAW77780, in
 CC which the N-terminus is joined to the C-terminus directly or via a
 CC linker, the polypeptide having new C- and N-termini at one of the
 CC positions indicated. Novel claimed multi-functional chimeric
 CC haematopoietic receptor agonists (see AAW77812-22) have the formula R1-L1
 CC -R2, R2-L1-R1, R1-R2 or R2-R1, where L is a linker and R1 and R2 are
 CC independently selected from: (a) the human EPO receptor agonist; (b) a
 CC human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a
 CC human flt-3 receptor agonist polypeptide (see AAW77782); (d) a modified
 CC human granulocyte colony stimulating factor (G-CSF) polypeptide (see
 CC AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784);
 CC (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a
 CC factor selected from the group consisting of a CSF, a cytokine, a
 CC lymphokine, an interleukin and a haematopoietic growth factor, provided
 CC that at least R1 or R2 is selected from (a), (b) or (c) as above. The
 CC multi-functional chimeric haematopoietic receptor agonist can be used to
 CC stimulate the production of haematopoietic cells in a patient, for the ex
 CC vivo expansion of haematopoietic cells, for the production of dendritic

Query Match 100.0%; Score 851; DB 2; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPTKYNFYANKMEVGGQA 60
 DB 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPTKYNFYANKMEVGGQA 60
 QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLLRALGAQKEAIS 120
 QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 166
 DB 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 166
 RESULT 5
 ABB07030
 ID ABB07030 standard; protein; 166 AA.
 XX
 AC ABB07030;
 XX
 DT 21-JUN-2002 (first entry)
 XX
 DE Modified erythropoietin related gene protein sequence.
 XX
 KW Modified erythropoietin; EPO.
 XX
 OS Unidentified.
 XX
 PN KR145802-B1.
 XX
 PD 01-AUG-1998.
 XX
 PF 31-MAY-1994; 94KR-00012082.
 XX
 PR 31-MAY-1994; 94KR-00012082.
 XX
 PA (GLDS) LG CHEM CO LTD.
 XX
 PI Kim C, Song Y, Lee T;
 XX
 DR WPI; 2000-234250/20.
 DR N-PSDB; ABL50878.
 XX
 PT MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF.
 XX
 PS Disclosure; Page 14; 15pp; Korean.
 CC
 CC The present invention describes modified erythropoietin (EPO) genes and
 CC expression vectors comprising the genes. The present sequence represents
 CC a protein sequence from the present invention
 XX
 SQ Sequence 166 AA;
 Query Match 100.0%; Score 851; DB 3; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPTKYNFYANKMEVGGQA 60
 DB 1 APPRLICDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPTKYNFYANKMEVGGQA 60
 QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLSLTLTLLRALGAQKEAIS 120
 QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 166
 DB 121 PPDAASAPLRTITADTFRKLFRVYSNFRGKLYTGACRTGDR 166

RESULT 6

ABB83622
ID ABB83622 standard; protein; 166 AA.
XX AC ABB83622;
XX DT 10-OCT-2002 (first entry)
XX DE Protein #2 relating to modified erythropoietin glycoprotein.
XX KW Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
XX OS cancer.
XX OS Unidentified.
XX PN NO200003372-A.
XX PD 03-JAN-2001.
XX PF 28-JUN-2000; 2000NO-00003372.
XX PR 02-JUL-1999; 99US-0142254P.
XX PR 23-AUG-1999; 99US-0150225P.
XX PR 31-AUG-1999; 99US-0151548P.
XX PR 17-NOV-1999; 99US-0166151P.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PI Bailon PS;
XX DR WFI; 2001-135308/14.
XX PT New conjugate having modified erythropoietin glycoprotein useful for
XX PT stimulating red blood cell production and for treating diseases
XX PT correlated with anaemia in chronic renal failure, AIDS or cancer patients.
XX PS Disclosure; Page 22-23; 30pp; Norwegian.
XX CC This invention relates to new conjugate having a modified erythropoietin
XX CC glycoprotein, useful for stimulating red blood cell production, and for
XX CC treating or preventing diseases correlated with anaemia in chronic renal
XX CC failure, AIDS or cancer patients. The present sequence is a protein
XX CC related to the invention
XX SQ Sequence 166 AA;
Query Match 100.0%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.4e-87;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSITLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSITLLRALGAKKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
RESULT 7
AAE02641
XX ID AAE02641 standard; protein; 166 AA.
XX AC AAE02641;
XX DT 06-AUG-2001 (first entry)
XX DE Human erythropoietin (EPO) mature protein.
XX KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
KW vaccine; haemostatic; immunoglobulin; Ig; EPO deficient disease; anaemia;
renal failure; Human immunodeficiency Virus; HIV;
haematopoietic growth factor.
OS Homo sapiens.
XX WO200136489-A2.
XX PD 25-MAY-2001.
XX PF 03-NOV-2000; 2000WO-EP010843.
XX PR 12-NOV-1999; 99US-0164855P.
XX PA (MERE) MERCK PATENT GMBH.
XX PI Hartmann A, Brandt S, Riecke E, Sobel C, Lo K, Way JC, Gillies S;
XX DR WPI; 2001-367563/38.
XX DR N-PSDB; AAD06893.
XX PT Novel modified erythropoietin forms such as fusion proteins, comprising
XX PT Fc portion of an immunoglobulin molecule and a target molecule having the
XX PT biological activity of erythropoietin forms.
XX PS Example 1; Page 22; 58pp; English.
XX CC The present sequence is human erythropoietin (EPO) mature protein. EPO
XX CC has improved biological activity and an extended serum half life greater
XX CC than 20 hours. The present invention relates to modified EPO forms such
XX CC as fusion proteins comprising a Fc portion of an immunoglobulin (Ig)
XX CC molecule and an EPO molecule (Fc-EPO). The Fc portion is fused covalently
XX CC through its C-terminus directly or indirectly to the EPO molecule, and
XX CC where the Fc portion as well as EPO portion may be modified or mutated.
XX CC The invention also relates to non-fused EPO molecules which have a
XX CC pattern of cysteines or disulphide bonding which is distinct from human
XX CC or animal EPO. Pharmaceutical compositions containing EPO are useful in
XX CC the treatment of EPO deficient diseases such as anaemia, renal failure,
XX CC HIV infection, blood loss and chronic disease that can be treated with
XX CC haematopoietic growth factor
XX SQ Sequence 166 AA;
Query Match 100.0%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.4e-87;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGQQA 60
Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSITLLRALGAKKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSITLLRALGAKKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
RESULT 8
AAB66698
XX ID AAB66698 standard; protein; 166 AA.
XX AC AAB66698;
XX DT 06-APR-2001 (first entry)
XX DE Human erythropoietin protein #2.
XX KW Erythropoietin; EPO; reticulocytes; red blood cell; ethylene glycol;
XX KW chronic renal failure; AIDS; cancer.

FT Modified-site 83
 FT Modified-site /note= "N-glycosylated"
 FT 126
 FT Modified-site /note= "O-glycosylated"
 FT 126
 FN WO200187329-A1.
 FN 22-NOV-2001.
 FN 08-MAY-2001; 2001WO-EP005187.
 FN 15-MAY-2000; 2000EP-00110355.
 FN (HOFF) HOFFMANN LA ROCHE & CO AG F.
 FN Papadimitriou A;
 FN WPI; 2002-082943/11.
 FN Composition useful in the treatment of e.g. AIDS comprises an erythropoietin protein, and a multiple charged inorganic anion in a buffer.
 FN Claim 28; Fig 2; 64pp; English.
 FN The invention relates to liquid pharmaceutical compositions comprising an erythropoietin (EPO) protein, a multiple negatively charged inorganic anion in a buffer which maintains the pH of the solution from 5.5-7.0, and optionally at least one excipient. The erythropoietin used in the composition is preferably human (AM53061 or AM53062) a human erythropoietin variant containing additional glycosylation sites (AM53064-AM53107), or an erythropoietin with the C-terminal addition of a C-terminal fragment of human chorionic gonadotropin (AM53063).
 FN Erythropoietin is a glycoprotein essential for the formation of red blood cells and is therefore useful in the treatment of blood disorders characterised by low or defective red blood cell production. The compositions of the invention can be used in the treatment and prevention of anaemia in chronic renal failure patients (CRF), AIDS (acquired immunodeficiency syndrome), and/or for the treatment of cancer patients undergoing chemotherapy. Unlike prior art erythropoietin compositions, the compositions of the invention do not contain human serum albumin (thereby avoiding the possibility of viral infections and allergic reactions associated with this component), are liquid rather than lyophilisates (and therefore do not need to be reconstituted before administration), and are stable at elevated temperatures such as 25 degrees Celsius and even 40 degrees Celsius, and therefore can be stored without refrigeration for prolonged periods without degradation and loss of activity. The present sequence represents the 166 residue form of human erythropoietin which is specifically claimed for use in a composition of the invention
 SQ Sequence 166 AA;
 Query Match 100.0%; Score 851; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRLLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
 Db 1 APRLLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
 QY 1 APRLLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
 Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYLTGEACRTGDR 166
 QY 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYLTGEACRTGDR 166
 Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYLTGEACRTGDR 166
 RESULT 11
 ABB77897
 ID ABB77897 standard; protein; 166 AA.

XX ABB77897;
 XX 07-OCT-2002 (first entry)
 XX Amino acid sequence of a human erythropoietin (EPO).
 XX Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 OS Homo sapiens.
 XX WO200249673-A2.
 XX 27-JUN-2002.
 XX 08-DEC-2001; 2001WO-EP014434.
 XX 20-DEC-2000; 2000EP-00127891.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischner W;
 PI Wozny M;
 XX WPI; 2002-566640/60.
 XX Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
 XX Claim 26; Fig 2; 40pp; English.
 XX The present sequence represents a human erythropoietin (EPO) protein. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
 SQ Sequence 166 AA;
 Query Match 100.0%; Score 851; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRLLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
 Db 1 APRLLCDSRVLYRYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLQLHVDKAVSGLSRLTLLRALGAKQEAIS 120
 QY 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYLTGEACRTGDR 166
 Db 121 PPDAASAAPLRTITADTFKRLFRVYNSFLRGKLYLTGEACRTGDR 166
 RESULT 12

ADG55661
ID ADG55661 standard; protein; 166 AA.
XX
AC ADG55661;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human erythropoietin.
XX
KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
KW immunogenicity; MHC class II; antibody.
XX
OS Homo sapiens.
XX
PN WO200269232-A2.
XX
PD 06-SEP-2002.
XX
PF 18-FEB-2002; 2002WO-EP001688.
XX
PR 19-FEB-2001; 2001EP-00103954.
PR 08-MAR-2001; 2001EP-00103777.
PR 15-MAR-2001; 2001EP-00105336.
PR 20-MAR-2001; 2001EP-00106538.
PR 20-MAR-2001; 2001EP-00106899.
PR 20-MAR-2001; 2001EP-00107012.
PR 27-MAR-2001; 2001EP-00107568.
PR 25-APR-2001; 2001EP-00110220.
PR 30-MAY-2001; 2001EP-00113228.
PR 19-OCT-2001; 2001EP-00124965.
PR 12-NOV-2001; 2001EP-00126859.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
DR WPI; 2002-750424/81.
XX
PT Identifying potential T-cell epitope peptides within the amino acid
PT sequence of a biological molecule, useful for preparing a biological
PT molecule with reduced immunogenicity, comprises determining peptide
PT binding to MHC molecules.
XX
PS Example 7; Page 36; 85pp; English.
XX
CC The invention relates to a novel method for identifying one or more
CC potential T-cell epitope peptides within the amino acid sequence of a
CC biological molecule by determining the binding of the peptides to major
CC histocompatibility complex (MHC) molecules using in vitro or in silico
CC techniques or biological assays. The method of the invention is useful
CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
CC their fragments with reduced immunogenicity. The potential T-cell epitope
CC peptide within the amino acid sequence of a parent immunogenically non-
CC modified biological molecule identified is useful for preparing a
CC biological molecule with reduced immunogenicity and having a retained
CC desired biological activity, where the T-cell epitope is a 13mer peptide.
CC The present sequence is used in the exemplification of the invention.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 851; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.4e-87;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDRVLYRLLYLEAKEENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 60
DB 1 APPRLCDRVLYRLLYLEAKEENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 60
QY 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQHLVDKAVSGLSRLTLLRALGAQKEATS 120
DB 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQHLVDKAVSGLSRLTLLRALGAQKEATS 120
QY 121 PPDAASAPLRTTADTFRKLFRVYSNLFGLKLYTGACRTGDR 166

DB 121 PPDAASAPLRTTADTFRKLFRVYSNLFGLKLYTGACRTGDR 166
RESULT 13
ABR39996
ID ABR39996 standard; protein; 166 AA.
XX
AC ABR39996;
XX
DT 02-SEP-2003 (first entry)
XX
DE Human erythropoietin (EPO) sequence.
XX
KW EPO; erythropoietin; muten; reticulocyte; red blood cell; antianemic;
KW AIDS; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 7..161 /note= "disulphide bridge"
FT Disulfide-bond 29..33 /note= "disulphide bridge"
FT Modified-site 38 /note= "Asn is N-glycosylated"
FT Modified-site 83 /note= "Asn is N-glycosylated"
FT Modified-site 126 /note= "Ser is O-glycosylated"
XX
PN WO2003029291-A2.
XX
PD 10-APR-2003.
XX
PF 20-SEP-2002; 2002WO-EP010556.
XX
PR 25-SEP-2001; 2001EP-00122555.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Tischer W;
XX
DR WPI; 2003-457226/43.
XX
PT Novel erythropoietin muten having in vivo biological activity of causing
PT bone marrow cells to increase production of reticulocytes/red blood
PT cells, is N-glycosylated at Asn38 and Asn83 but not N-glycosylated at
PT Asn24.
XX
PS Claim 6; Page 22; 22pp; English.
XX
CC The invention relates to an erythropoietin muten (I) having the in vivo
CC biological activity of causing bone marrow cells to increase production
CC of reticulocytes and red blood cells, characterized by being N-
CC glycosylated at Asn38 and Asn83 but not N-glycosylated at Asn24. (I) or
CC an aqueous composition comprising an erythropoietin muten is useful for
CC the preparation of a medicament for the treatment or prophylaxis of
CC diseases correlated with anemia in chronic renal failure patients (CRF),
CC AIDS and for the treatment of cancer patients undergoing chemotherapy.
CC (I) or the composition is useful for treating a human patient
CC experiencing blood disorders characterized by low or defective red blood
CC cell production. (I) is useful for enhancing red blood cell formation.
CC The present sequence represents a human erythropoietin (EPO) sequence
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 851; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.4e-87;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDRVLYRLLYLEAKEENITTCGAHCSLNENITVPDTKNFYAWKMEVGOQA 60

Db 1 APPRLICDSRVRLRYLLLEAKAEENITTCAGHCSLNENITVDTKKNFYAKRMEVGGQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLTTLRLALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLTTLRLALGAQKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 14
ABR57500
ID ABR57500 standard; protein; 166 AA.
AC ABR57500;

DT 19-SEP-2003 (first entry)

DE Human erythropoietin (EPO) amino acid sequence SEQ ID NO:1.

XX Human; erythropoietin; EPO; hEPO; tranquilliser; cerebroprotective;
XX anticonvulsant; vasotropic; antiinflammatory; immunosuppressive;
XX antianemic; antirheumatic; antiarthritic; anti-HIV; nephrotropic;
XX red blood cell production stimulator; head trauma; stroke; epilepsy;
XX ischaemia; hypoxia; immune-mediated inflammation; CNS disorder; HIV;
XX excessive neuronal excitation; central nervous system disorder;
XX chronic renal failure; anaemia; chronic inflammatory disease;
XX rheumatoid arthritis.

XX Homo sapiens.

XX WO2003055526-A2.

XX 10-JUL-2003.

XX 18-DEC-2002; 2002WO-DK000871.

XX 21-DEC-2001; 2001DK-00001953.

XX 21-DEC-2001; 2001US-0343501P.

XX (MAXY-) MAXYGEN APS.

XX (MAXY-) MAXYGEN HOLDINGS LTD.

XX Andersen KV;

XX WPI; 2003-577388/54.

XX Polypeptide conjugate useful in the treatment of e.g. stroke, head trauma
XX and hypoxia comprises polymer molecule covalently attached to attachment
XX site of human erythropoietin-like polypeptide.

XX Disclosure; Page 61-62; 62pp; English.

XX The present invention describes a polypeptide conjugate (I), which
XX comprises at least one polymer molecule (a) covalently attached to an
XX attachment site of a human erythropoietin-like polypeptide (b), where (b)
XX comprises at least one removed and/or introduced lysine, cysteine,
XX aspartic acid or glutamic acid residue compared to the amino acid
XX sequence of human erythropoietin (hEPO). Also described: (1) a
XX polypeptide comprising the amino acid sequence of (b); and (2) use of (I)
XX as a pharmaceutical and in the preparation of a medicament for the
XX prevention or treatment of disorders involving low or defective red blood
XX cell production. (I) has tranquilliser, cerebroprotective,
XX anticonvulsant, vasotropic, antiinflammatory, immunosuppressive,
XX antianemic, antirheumatic, antiarthritic, anti-HIV and nephrotropic
XX activities, and can be used as a red blood cell production stimulator.
XX (I) can be used as a pharmaceutical; in the manufacture of a medicament
XX for prevention or treatment of disorders involving low or defective red
XX blood cell production; and in the treatment of head trauma, stroke,
XX epilepsy, ischaemia, hypoxia, immune-mediated inflammation, excessive
XX neuronal excitation and other central nervous system (CNS) related
XX conditions. Also useful for the treatment of HIV, chronic renal failure,

CC anaemia in patients with non-myeloid malignancies, chronic inflammatory
CC disease e.g. rheumatoid arthritis, anaemia associated with chronic
CC disease, senile anaemia and anaemia in patients undergoing blood
CC transfusion. The present sequence represents hEPO, which is given in the
CC exemplification of the present invention

SQ Sequence 166 AA;

Query Match 100.0%; Score 851; DB 6; Length 166;

Best Local Similarity 100.0%; Pred. No. 7.4e-87;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVRLRYLLLEAKAEENITTCAGHCSLNENITVDTKKNFYAKRMEVGGQA 60

Db 1 APPRLICDSRVRLRYLLLEAKAEENITTCAGHCSLNENITVDTKKNFYAKRMEVGGQA 60

Qy 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLTTLRLALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRQALLVNSQWPEPLQLHVDKAVSGLSLTTLRLALGAQKEAIS 120

Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166

Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166

RESULT 15

ADF70839

ID ADF70839 standard; protein; 166 AA.

XX ADF70839;

XX 12-FEB-2004 (first entry)

XX Human erythropoietin (EPO).

XX immunostimulant; granulocyte macrophage colony stimulating factor;

XX GM-CSF; neutropenia; myelosuppressive chemotherapy;

XX bone marrow transplantation; HIV infection; burn; surgery; dilatation;

XX anaemia; neonatal septicaemia; severe chronic neutropenia;

XX aplastic anaemia; acute leukaemia; human; growth hormone super family;

XX erythropoietin; EPO.

XX Homo sapiens.

XX US2003171284-A1.

XX 11-SEP-2003.

XX 15-NOV-2002; 2002US-00298148.

XX 14-JUL-1997; 97US-0052516P.

XX 13-JUL-1998; 98WO-US014497.

XX 14-JAN-2000; 2000US-00462941.

XX 15-NOV-2001; 2001US-0332285P.

XX 11-OCT-2002; 2002US-0418040P.

XX (COXG/) COX G N.

XX (DOHE/) DOHERTY D H.

XX Cox GN, Doherty DH;

XX WPI; 2003-898295/82.

XX Protecting an animal from a disease or condition, useful for treating
XX neutropenia, comprises administering to an animal having the disease or
XX condition a composition comprising GM-CSF cysteine mutein.

XX Example 2; SEQ ID NO 2; 56pp; English.

XX The invention describes protecting an animal from a disease or condition
XX that can be treated by wild-type granulocyte macrophage colony
XX stimulating factor (GM-CSF) comprising administering to an animal having
XX the disease or condition a composition comprising GM-CSF cysteine mutein.

CC The methods are useful for preventing or treating the occurrence of
 CC neutropenia in an animal, the neutropenia is selected from neutropenia
 CC resulting from myelosuppressive chemotherapy, neutropenia associated with
 CC bone marrow transplantation, neutropenia associated with infection with
 CC the human immunodeficiency virus, neutropenia associated with burns,
 CC surgery, dilatation, anaemia and neonatal septicemia, severe chronic
 CC neutropenia, neutropenia associated with aplastic anaemia and acute
 CC leukaemia. This is the amino acid sequence of human erythropoietin (EPO),
 CC a member of the growth hormone super family which also includes
 CC interleukins.
 XX
 SQ Sequence 166 AA;

Query Match 100.0%; Score 851; DB 7; Length 166;
 Best Local Similarity 100.0%; Pred. No. 7.4e-87;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRLICDSRLRYLLLEAKEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
 DB 1 APPRLICDSRLRYLLLEAKEENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLRSLTTLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLRSLTTLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFKLFVYSNLFGRGKLYTGEACRTGDR 166
 DB 121 PPDAASAAPLRTITADTFKLFVYSNLFGRGKLYTGEACRTGDR 166

Search completed: December 3, 2004, 13:34:06
 Job time : 63.6888 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:23:08 ; Search time 19,0574 Seconds
(without alignments)
577.665 Million cell updates/sec

Title: US-10-780-297-2

Perfect score: 851

Sequence: 1 APPRLICDSRVLELYLEAK.....NFLRGKLYTGCACTGDR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfilee1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	166	1	US-08-318-193-70
2	851	100.0	166	3	US-09-604-871-2
3	851	100.0	166	4	US-09-604-938-2
4	851	100.0	166	4	US-09-462-941-2
5	851	100.0	166	5	PCT-US94-04361-37
6	851	100.0	193	1	US-07-903-220-1
7	851	100.0	193	2	US-08-883-795A-34
8	851	100.0	193	4	US-09-552-265B-4
9	848	99.6	412	4	US-09-366-009-34
10	848	99.6	412	4	US-08-909-156B-34
11	846	99.4	165	3	US-09-604-871-1
12	846	99.4	165	4	US-09-604-938-1
13	846	99.4	165	4	US-09-830-967-1
14	843	99.1	165	4	US-09-554-451-8
15	843	99.1	193	4	US-09-552-265B-2
16	839	98.6	193	4	US-09-552-265B-5
17	835	98.1	166	5	PCT-US94-04361-45
18	830	97.5	166	4	US-09-552-265B-30
19	830	97.5	193	4	US-09-552-265B-46
20	829	97.4	166	4	US-09-552-265B-22
21	829	97.4	166	4	US-09-552-265B-32
22	829	97.4	193	4	US-09-552-265B-38
23	829	97.4	193	4	US-09-552-265B-48
24	827	97.2	166	4	US-09-552-265B-20
25	827	97.2	166	4	US-09-552-265B-24
26	827	97.2	193	4	US-09-552-265B-36
27	827	97.2	193	4	US-09-552-265B-40

28	826	97.1	166	4	US-09-552-265B-26	Sequence 26, Appl
29	826	97.1	166	4	US-09-552-265B-31	Sequence 31, Appl
30	826	97.1	193	4	US-09-552-265B-42	Sequence 42, Appl
31	826	97.1	193	4	US-09-552-265B-47	Sequence 47, Appl
32	825	96.9	166	4	US-09-552-265B-18	Sequence 18, Appl
33	825	96.9	166	4	US-09-552-265B-23	Sequence 23, Appl
34	825	96.9	166	4	US-09-552-265B-28	Sequence 28, Appl
35	825	96.9	166	4	US-09-552-265B-33	Sequence 33, Appl
36	825	96.9	193	4	US-09-552-265B-34	Sequence 34, Appl
37	825	96.9	193	4	US-09-552-265B-39	Sequence 39, Appl
38	825	96.9	193	4	US-09-552-265B-44	Sequence 44, Appl
39	825	96.9	193	4	US-09-552-265B-49	Sequence 49, Appl
40	823	96.7	166	4	US-09-552-265B-21	Sequence 21, Appl
41	823	96.7	166	4	US-09-552-265B-25	Sequence 25, Appl
42	823	96.7	193	4	US-09-552-265B-37	Sequence 37, Appl
43	823	96.7	193	4	US-09-552-265B-41	Sequence 41, Appl
44	822	96.6	166	4	US-09-552-265B-27	Sequence 27, Appl
45	822	96.6	193	4	US-09-552-265B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-70

Query Match 100.0%; Score 851; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;

```
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2
Query Match 100.0%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
RESULT 2
US-09-604-871-2
; Sequence 2, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Josel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-2
Query Match 100.0%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
RESULT 3
US-09-604-938-2
; Sequence 2, Application US/09604938
; Patent No. 6583272
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
```

```
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-938-2
Query Match 100.0%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
RESULT 4
US-09-462-941-2
; Sequence 2, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder, Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-2
Query Match 100.0%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
DB 1 APPRLICDSRVLYRLLLEAKEAENITTCAGHCSLNENITVPDTKVFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
DB 121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKGLKLYTGEACRTGDR 166
RESULT 5
PCT-US94-04361-37
; Sequence 37, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
```

APPLICANT: Bunn, H. Franklin
 APPLICANT: Wen, Dany
 APPLICANT: Showers, Mark O.
 TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
 TITLE OF INVENTION: Activity
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04361
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/049,802
 FILING DATE: 21-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Cimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0627.336PC01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 PCT-US94-04361-37

Query Match 100.0%; Score 851; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 3.5e-100;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 DB 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 120
 QY 121 PDAAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 166
 DB 121 PDAAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 166

RESULT 6
 US-07-903-220-1
 Sequence 1, Application US/07903220
 Patent No. 532837
 GENERAL INFORMATION:
 APPLICANT: Hewick, Rodney M.
 TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
 TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Paul H. Heller
 STREET: Kenyon & Kenyon, One Broadway
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10004
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/903,220
 FILING DATE: 19920731
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: 1248/27
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 429-1776
 TELEFAX: (202) 429-0796
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 193 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-07-903-220-1
 Query Match 100.0%; Score 851; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 4.4e-100;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
 DB 28 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 87
 QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 120
 DB 88 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLLTLRALGAQKEAIS 147
 QY 121 PDAAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 166
 DB 148 PDAAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGDR 193

RESULT 7
 US-08-883-795A-34
 Sequence 34, Application US/08883795A
 Patent No. 5985607
 GENERAL INFORMATION:
 APPLICANT: Delcuve, Genevieve
 APPLICANT: Awang, Gregor
 TITLE OF INVENTION: Recombinant DNA Molecules and Expression
 TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/883,795A
 FILING DATE: 27-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gravelle, Micheline
 REGISTRATION NUMBER: 40,261
 REFERENCE/DOCKET NUMBER: 7841-062

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-883-795A-34
;
Query Match 100.0%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.4e-100; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0;
;
QY 1 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 60
DB 28 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 193
;
RESULT 8
US-09-552-265B-4
; Sequence 4, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-265B-4
;
Query Match 100.0%; Score 851; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.4e-100; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 0;
;
QY 1 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 60
DB 28 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 193
;
RESULT 9
US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Ueno, Takashi
```

```
;
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
;
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34
;
Query Match 99.6%; Score 848; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 3.6e-99;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 60
DB 233 APPRLICDSRVLYRLLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAKRMEVGGQA 292
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 293 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 352
QY 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 166
DB 353 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLYTGEACRTGDR 398
;
RESULT 10
US-08-809-156B-34
; Sequence 34, Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; APPLICANT: Uemori, Takashi
; APPLICANT: Ueno, Takashi
```

APPLICANT: Koyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunshizu
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-34

Query Match 99.6%; Score 848; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 3.6e-99;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 233 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 292
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 120
Db 293 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 352
Qy 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 166
Db 353 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGDR 398

RESULT 11
US-09-604-871-1
Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/142,243
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-871-1

Query Match 99.4%; Score 846; DB 3; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 120
Qy 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165

RESULT 12
US-09-604-938-1
Sequence 1, Application US/09604938
Patent No. 6583272
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/150,225
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 165
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-938-1

Query Match 99.4%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Db 1 APPLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKKNFYAKRMEVGQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAKAEALS 120
Qy 121 PPDAASAAPLRTITADTFRKLFVYSNFRGLKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 13

US-09-830-967-1

; Sequence 1, Application US/09930967

; Patent No. 6777205

; GENERAL INFORMATION:

; APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.

; APPLICANT: Carcagno, Carlos Miguel

; APPLICANT: Criscuolo, Marcelo

; APPLICANT: Melo, Carlos

; APPLICANT: Vidal, Juan Alejandro

; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin

; FILE REFERENCE: 1909.0020002

; CURRENT APPLICATION NUMBER: US/09/830,967

; CURRENT FILING DATE: 1999-11-08

; PRIOR APPLICATION NUMBER: AR 99-01-00679

; PRIOR FILING DATE: 1999-02-23

; PRIOR APPLICATION NUMBER: AR 98-01-05609

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 1

; LENGTH: 165

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-830-967-1

Query Match 99.4%; Score 846; DB 4; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.5e-99;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 60

Db 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 60

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 14

US-09-554-451-8

; Sequence 8, Application US/09554451

; Patent No. 6680207

; GENERAL INFORMATION:

; APPLICANT: Jonathan Paul MURPHY

; APPLICANT: Anthony ATKINSON

; TITLE OF INVENTION: Detection of Molecules in Samples

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Winthrop, L.L.P.

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/554,451

; FILING DATE: 15-May-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/03449

; FILING DATE: No. 6680207ember 16, 1998

; APPLICATION NUMBER: GB 9723955.2

; FILING DATE: No. 6680207ember 14, 1997

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 165 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-554-451-8

Query Match 99.1%; Score 843; DB 4; Length 165;

Best Local Similarity 99.4%; Pred. No. 3.6e-99;

Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 60

Db 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 60

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 15

US-09-552-265B-2

; Sequence 2, Application US/09552265B

; Patent No. 6555343

; GENERAL INFORMATION:

; APPLICANT: DeSavage, Frederick

; APPLICANT: Henner, Dennis, J.

; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)

; FILE REFERENCE: polypeptides and nucleic acids encoding the same

; CURRENT APPLICATION NUMBER: US/09/552,265B

; CURRENT FILING DATE: 2000-04-19

; PRIOR APPLICATION NUMBER: US 09/307307

; PRIOR FILING DATE: 1999-05-17.

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Pan troglodytes

US-09-552-265B-2

Query Match 99.1%; Score 843; DB 4; Length 193;

Best Local Similarity 99.4%; Pred. No. 4.6e-99;

Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 60

Db 28 APPRLICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKNFYANKRMEVGGQA 87

QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120

Db 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHVDKAVSGLSLTLRLALGAQKEAIS 147

QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 166

Db 148 PPDAASAAPLRTITADTFKFLFRVYSNFLRGKLYTGEACRTGD 193

Search completed: December 3, 2004, 13:39:28

Job time : 20.0574 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:28:44 ; Search time 51.1541 Seconds
(without alignments)
1157.277 Million cell updates/sec

Title: US-10-780-297-2

Perfect score: 851

Sequence: 1 APPLICDSRVLYLEAKE.....NFLRGKLYTGACRTGDR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 segs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	166	9	US-09-853-731-2
2	851	100.0	166	13	Sequence 2, Appli
3	851	100.0	166	14	US-10-014-363-2
4	851	100.0	166	14	US-10-241-356-2
5	851	100.0	166	14	US-10-293-551-2
6	851	100.0	166	14	US-10-400-377-2
7	851	100.0	166	14	US-10-400-708-2
8	851	100.0	166	14	US-10-298-148-2
9	851	100.0	166	15	US-10-360-101-227
10	851	100.0	166	15	US-10-467-115-1
11	851	100.0	166	16	US-10-658-834A-201
12	851	100.0	166	16	US-10-773-939-2
13	851	100.0	166	16	US-10-774-149-2
					Sequence 133, App

14	851	100.0	166	17	US-10-773-654-2	Sequence 2, Appli
15	851	100.0	166	17	US-10-866-540-2	Sequence 2, Appli
16	851	100.0	169	13	US-10-014-363-3	Sequence 4, Appli
17	851	100.0	174	13	US-10-014-363-3	Sequence 3, Appli
18	851	100.0	174	13	US-10-014-363-5	Sequence 5, Appli
19	851	100.0	193	10	US-09-813-775C-4	Sequence 4, Appli
20	851	100.0	193	14	US-10-113-824-2	Sequence 2, Appli
21	851	100.0	193	16	US-10-612-665-10	Sequence 10, Appli
22	851	100.0	193	16	US-10-612-665-22	Sequence 22, Appli
23	851	100.0	193	16	US-10-612-665-112	Sequence 112, App
24	851	100.0	193	17	US-10-676-694-10	Sequence 10, Appli
25	851	100.0	193	17	US-10-676-694-22	Sequence 22, Appli
26	851	100.0	193	17	US-10-676-694-112	Sequence 112, App
27	851	100.0	428	14	US-10-435-608-10	Sequence 10, Appli
28	851	100.0	428	15	US-10-822-108-10	Sequence 10, Appli
29	850	99.9	194	17	US-10-637-313-102	Sequence 102, App
30	849	99.8	166	16	US-10-658-834A-959	Sequence 959, App
31	849	99.8	166	16	US-10-658-834A-957	Sequence 957, App
32	848	99.6	166	16	US-10-658-834A-952	Sequence 952, App
33	848	99.6	166	16	US-10-658-834A-955	Sequence 955, App
34	848	99.6	166	16	US-10-658-834A-958	Sequence 958, App
35	848	99.6	166	16	US-10-658-834A-966	Sequence 966, App
36	848	99.6	193	14	US-10-435-608-4	Sequence 4, Appli
37	848	99.6	193	15	US-10-622-108-4	Sequence 4, Appli
38	848	99.6	193	16	US-10-612-665-63	Sequence 63, Appli
39	848	99.6	193	16	US-10-612-665-64	Sequence 64, Appli
40	848	99.6	193	16	US-10-612-665-70	Sequence 70, Appli
41	848	99.6	193	16	US-10-612-665-81	Sequence 81, Appli
42	848	99.6	193	16	US-10-612-665-88	Sequence 88, Appli
43	848	99.6	193	16	US-10-612-665-91	Sequence 91, Appli
44	848	99.6	193	17	US-10-676-694-63	Sequence 63, Appli
45	848	99.6	193	17	US-10-676-694-64	Sequence 64, Appli

ALIGNMENTS

RESULT 1
US-09-853-731-2
; Sequence 2, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853.731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-2

Query Match 100.0%; Score 851; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	APPLICDSRVLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKEVQCOA	60
Db	1	APPLICDSRVLYLEAKEAENITTCGAHCSLNENITVPDTKNFYAWKEVQCOA	60
Qy	61	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS	120
Db	61	VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSLTTLRALGAQKEAIS	120
Qy	121	PDMAASAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR	166
Db	121	PDMAASAPLRTITADTFRKLFRVYNSFLRGKLYTGACRTGDR	166

121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
RESULT 4
US-10-293-551-2
; Sequence 2, Application US/10293551
; Publication No. US20030120045A1
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-2
Query Match 100.0%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
DB 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
DB 121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
RESULT 5
US-10-400-377-2
; Sequence 2, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-2

US-10-014-363-2
; Sequence 2, Application US/10014363
; Publication No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-2
Query Match 100.0%; Score 851; DB 13; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
DB 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120
QY 121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
DB 121 PPDAASAPLRTITADTFRKLFRVYSNFRGLKLYTGACRTGDR 166
RESULT 3
US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2
Query Match 100.0%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
DB 1 APPRLCDSRVLYRLLYLLAKEAENITTCGAHCSLNENITVPDTKNFYANKMEVGOQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQFWPEPLQHVDKAVSGLSLTLRLALGAQKEAIS 120


```
Query Match      100.0%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 6
US-10-400-708-2
; Sequence 2, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-2

Query Match      100.0%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 7
US-10-298-148-2
; Sequence 2, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
```

```
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-2

Query Match      100.0%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 8
US-10-360-101-227
; Sequence 227, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N
; APPLICANT: Leenhouts, Cornelis J
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2193-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227

Query Match      100.0%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCAGHCSLNENITVPDTKNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 9
US-10-467-115-1
; Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
```

```

; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
; FILE REFERENCE: REDUCED IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/467,115
; PRIOR FILING DATE: 2003-08-05
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-06
; PRIOR FILING DATE: 2001-02-19
; PRIOR FILING DATE: 2001-02-19
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-115-1

Query Match      100.0%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 11
US-10-773-939-2
; Sequence 2, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/773,939
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-939-2

Query Match      100.0%; Score 851; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

RESULT 12
US-10-774-149-2
; Sequence 2, Application US/10774149
; Publication No. US20040175800A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/774,149
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

Query Match      100.0%; Score 851; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPWEPLOLHVVDKAVSGLSRSLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYSNFRGKLYTGACRTGDR 166

US-10-658-834A-201
; Sequence 201, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA52400
; DATABASE ENTRY DATE: 1994-11-08
US-10-658-834A-201

Query Match      100.0%; Score 851; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.2e-86;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNLENITVPDTKKNFYANKRMEVGQQA 60
```

```

; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-774-149-2

Query Match
Best Local Similarity 100.0%; Score 851; DB 16; Length 166;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPTKVNFYAWKMEVGQQA 60
DB 1 APPRLCDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPTKVNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGCAKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGCAKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGCACTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGCACTGDR 166

RESULT 13
US-10-468-496-133
; Sequence 133, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Cart, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-468-496-133

Query Match
Best Local Similarity 100.0%; Score 851; DB 16; Length 166;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPTKVNFYAWKMEVGQQA 60
DB 1 APPRLCDSRVLYRLLLEAKAEENITTCGAHCSLNENITVPTKVNFYAWKMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGCAKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTTLRALGCAKEAIS 120
QY 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGCACTGDR 166
DB 121 PPDAASAAPLRTITADTFKFLFRVYNSFLRGKLYTGCACTGDR 166

```

Qy	1	APPRICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA	60
Db	1	APPRICDSRVLERYLLEAKEAENITTCGAHCSLNENITVPDTKVFYAWKMEVGQQA	60
Qy	61	VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVHDKAVSGLRSLTTLRLALGACKKAIS	120
Db	61	VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQHVHDKAVSGLRSLTTLRLALGACKKAIS	120
Qy	121	PDRAASAPLRTITADTFRKLFRVYSNFRGKLYTGCACTGDR	166
Db	121	PDRAASAPLRTITADTFRKLFRVYSNFRGKLYTGCACTGDR	166

Search completed: December 3, 2004, 13:41:16
Job time : 52.1541 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:09:33 ; Search time 13.0393 Seconds
(without alignments)
1224.913 Million cell updates/sec

Title: US-10-780-297-2

Perfect score: 851

Sequence: 1 APRRLICDSVLEYLEAK.....NPLRGKLYTGACRTGDR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	193	1 ZUHU	erythropoietin pre
2	769.5	90.4	192	1 JQ0173	erythropoietin pre
3	764.5	89.8	192	1 I84613	erythropoietin pre
4	718	84.4	188	1 I46083	erythropoietin pre
5	705	83.0	192	1 S28148	erythropoietin pre
6	690.5	81.1	194	1 I46401	erythropoietin pre
7	686	80.6	192	1 A24902	erythropoietin pre
8	685.5	80.6	195	2 JC7699	erythropoietin - r
9	683	80.3	190	2 I46578	erythropoietin - p
10	638	75.0	175	2 I46199	erythropoietin - d
11	90	10.6	333	2 G02729	thrombopoietin - h
12	89	10.5	333	2 I80105	thrombopoietin - h
13	88	10.3	332	2 AB0323	thrombopoietin - h
14	87.5	10.3	346	2 AE0959	thrombopoietin pre
15	86	10.1	286	2 A55530	thrombopoietin pre
16	85	10.0	339	2 A83274	ribonucleoside-dip
17	83.5	9.8	296	2 A10443	Solute binding rec
18	80.5	9.5	303	1 GNMVJ8	megakaryocyte grow
19	79.5	9.3	1829	2 T35681	probable 2-hydroxy
20	79	9.3	480	2 T55639	probable polypeptin
21	78.5	9.2	813	2 AF0526	probable sensory h
22	78.5	9.2	897	2 A54696	ribosomal protein
23	78	9.2	348	2 T35450	ATP receptor subu
24	78	9.2	455	2 AG2919	ABC transporter AT
25	78	9.2	455	2 H97693	conserved hypothet
26	78	9.2	747	1 S36741	methylamine utiliz
27	77.5	9.1	242	2 AD1928	probable copper-tr
28	77	9.0	451	2 S75569	hypothetical prote
29	77	9.0	548	2 B84932	hypothetical prote
					60 kD chaperonin [

ALIGNMENTS

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C.Species: Homo sapiens (man)

C.Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C.Accession: A01855; A24744; A25384; A22210; S56178

R.Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; Seel

Nature 313, 806-810, 1985

A.Title: Isolation and characterization of genomic and cDNA clones of human erythropoietin

A.Reference number: A01855; MUID:85137899; PMID:3838366

A.Accession: A01855

A.Molecule type: mRNA; DNA

A.Residues: 1-193 <JAC>

A.Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158

R.Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.;

Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A.Title: Cloning and expression of the human erythropoietin gene.

A.Reference number: A24744; MUID:86067948; PMID:3865178

A.Accession: A24744

A.Molecule type: DNA

A.Residues: 1-193 <LIN>

A.Cross-references: GB:M11319; NID:g182197; PID:AAA52400.1; PID:g182198

R.Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A.Title: Structural characterization of human erythropoietin.

A.Reference number: A25384; MUID:86140080; PMID:3949763

A.Accession: A25384

A.Molecule type: protein

A.Residues: 28-86,'Q',87-193 <LAI>

A.Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid

A.Experimental source: urine

R.Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A.Title: Isolation of human erythropoietin with monoclonal antibodies.

A.Reference number: A22210; MUID:84135751; PMID:6698989

A.Accession: A22210

A.Molecule type: protein

A.Residues: 28-29,'X',31-33,'L',35-50,'X',52-53,'D',55,'G',57 <YAN>

R.Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A>Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured t

A.Reference number: S56178; MUID:95284365; PMID:7766897

A.Accession: S56178

A.Molecule type: protein

A.Residues: 28-33,'X',35-37 <WTS>

C.Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of

C.Genetics:

A:Gene: GDB:EPO

A:Cross-references: GDB:119110; OMIM:133170

A:Map position: 7q21.3-7q22.1

A:Introns: 5/1, 53/3, 82/3, 142/3

C:Function:

synbionin syml - p
bacterioferritin X
mandelate racemase
groEL protein - Ba
hypothetical prote
conserved hypothet
rTS beta (AF305057
ATP-dependent heli
RF2 protein - sain
thrombopoietin pre
ribonucleoside-dip
chaperonin, 60 kD
PSB1 protein - Co
probable transport
hypothetical prote

30	77	9.0	548	2	B42281
31	76.5	9.0	154	2	H82810
32	76.5	9.0	425	2	AE3465
33	75.5	8.9	544	2	S37039
34	75.5	8.9	637	2	S75772
35	74.5	8.8	400	2	AB2922
36	74.5	8.8	425	2	C97696
37	74.5	8.8	824	2	D64738
38	74	8.7	282	2	B37994
39	74	8.7	326	2	JC4125
40	74	8.7	335	2	AE3625
41	74	8.7	544	2	B82048
42	74	8.7	552	2	S39765
43	74	8.7	1089	2	S53978
44	74	8.7	1564	2	S55517
45	73.5	8.6	401	2	H83911

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-193/Product: erythropoietin #status experimental <MAT>
F:34-188,56-60/Disulfide bonds: #status experimental
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 9.7e-74;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 166
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: JQ0173
R:Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
Gene 44, 201-209, 1986
A:Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A:Reference number: JQ0173; MUID:87055236; PMID:2877922
A:Accession: JQ0173
A:Molecule type: mRNA
A:Residues: 1-192 <RES>
A:Cross-references: UNIPROT:P07865; GB:M18189; GB:M15818; GB:M18188; NID:9342
A:Experimental source: kidney
C:Comment: This protein is the principal hormone involved in the regulation of erythrocy
C:Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-192/Product: erythropoietin #status predicted <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 769.5; DB 1; Length 192;
Best Local Similarity 91.6%; Pred. No. 5.7e-66;
Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 166
DB 147 LPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 192

RESULT 3
184613
erythropoietin precursor - rhesus macaque

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-192/Product: erythropoietin #status predicted <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.4%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 4.5e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 82

C:Species: Macaca mulatta (rhesus macaque)
C:Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: 184613
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A:Reference number: 146083; MUID:93372347; PMID:8364201
A:Accession: 184613
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192 <RES>
A:Cross-references: UNIPROT:Q28513; GB:L10609; NID:9342095; PIDN:AAA36842.1; PID:9342096
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of

C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-192/Product: erythropoietin #status predicted <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.8%; Score 764.5; DB 1; Length 192;
Best Local Similarity 90.4%; Pred. No. 1.7e-65;
Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 166
DB 147 LPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 192

RESULT 4
146083
erythropoietin precursor - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: 146083
R:Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homolo
A:Reference number: 146083; MUID:93372347; PMID:8364201
A:Accession: 146083
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <WEN>
A:Cross-references: UNIPROT:P33708; GB:L10606; NID:933820; PIDN:AAA30807.1; PID:9163821
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of

C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-188/Product: erythropoietin #status predicted <MAT>
F:29-183,51-55/Disulfide bonds: #status predicted
F:46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.4%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 4.5e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 82

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-193/Product: erythropoietin #status experimental <MAT>
F:34-188,56-60/Disulfide bonds: #status experimental
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 851; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 9.7e-74;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 166
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 193

RESULT 2
JQ0173
erythropoietin precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: JQ0173
R:Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
Gene 44, 201-209, 1986
A:Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
A:Reference number: JQ0173; MUID:87055236; PMID:2877922
A:Accession: JQ0173
A:Molecule type: mRNA
A:Residues: 1-192 <LIN>
A:Cross-references: UNIPROT:P07865; GB:M18189; GB:M15818; GB:M18188; NID:9342
A:Experimental source: kidney
C:Comment: This protein is the principal hormone involved in the regulation of erythrocy
C:Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-192/Product: erythropoietin #status predicted <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 769.5; DB 1; Length 192;
Best Local Similarity 91.6%; Pred. No. 5.7e-66;
Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 87

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQWPEPLQLHVDKAVSGLSRLTTLRALGAQKEAIS 146

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 166
DB 147 LPDAASAAPLRTITADTFKRLFRVYSNFRGKLYTGACRTGDR 192

RESULT 3
184613
erythropoietin precursor - rhesus macaque

A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-192/Product: erythropoietin #status predicted <MAT>
F:34-187,56-60/Disulfide bonds: #status predicted
F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.4%; Score 718; DB 1; Length 188;
Best Local Similarity 84.3%; Pred. No. 4.5e-61;
Matches 140; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 60
DB 23 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYANKRMEVGQQA 82

Qy	61	VEVWGALILSSA	VRGQALLVNS	QQWPEIQL	HVDKAVG	LSRLTLL	RALGAQ	KEATIS	120
	:	:	:	:	:	:	:	:	
Db	83	VEVWGALILSSA	ILRGQALLVNS	QQSQSETQL	HVDKAVG	LSRLTLL	RALGAQ	KEATIS	142
	:	:	:	:	:	:	:	:	
Qy	121	PPDASAAPLRT	ITADTRKLV	RVYSNLF	RGLKLYT	GEACRT	GDR	166	
	:	:	:	:	:	:	:		
Db	143	LPBNSAAPLRT	FTVDTLCKL	FRIYSNLF	RGLKLYT	GEACRR	GDR	188	
	:	:	:	:	:	:	:		

RESULT 5
S28148 erythropoietin precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C/Accession: S28148; I62743
R/Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
Biochim. Biophys. Acta 1171, 99-102, 1992
A/Title: Nucleotide sequence of rat erythropoietin.
A/Reference number: S28148; MUID:93042015; PMID:1420369
A/Accession: S28148
A/Molecule type: mRNA
A/Residues: 1-192 <NAG>
A/Cross-references: UNIPROT:P29676; GB:D10763; NID:G220735; PIDN:BAA01593.1; PID:G220736
R/Wen, D.; Bolssel, J.
Blood 82, 1507-1516, 1993
A/Title: Erythropoietin structure-function relationships: High degree of sequence homology
A/Reference number: I46083; MUID:93372347; PMID:8364201
A/Accession: I62743
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 4-192 <RES>
A/Cross-references: GB:I10608; NID:G204060; PIDN:AAA41126.1; PID:G204061
C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver C
C/Function:
A/Description: the primary inducer of erythrocyte formation
C/Superfamily: erythropoietin
C/Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-26/Domain: signal sequence #status predicted <SIG>
F:7-192/product: erythropoietin #status predicted <MAT>
F:33-187,55-165/Disulfide bonds: #status predicted
F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	83.0%;	Score 706;	DB 1;	Length 192;
Best Local Similarity	82.5%;	Pred. No. 6.4e-60;		
Matches 137;	Conservative 13;	Mismatches 16;	Indels 0;	Gaps 0;
QY	1	APPRLICDSRVLERVILEAKEAENITTCGAHCSLSENTVPDTKKNFYAWKGMVEGQA	60	
Db	27	APPRLICDSRVLERVILEAKEAENITTCGAEGPRLSENTVPDTKKNFYAWKRMVBEQA	86	
QY	61	VEVWQGLALLSEAVLRGQALVNSSQPWEPLQLHVDKAVSGLSRLTTLRALCAQKEAIS	120	
Db	87	VEVWQGLSLLSEATILQAQALQANSQPPESILQLHDKAISGLRSLSLTVLTVCAQKELMS	146	
QY	121	PDPAASAPLTIATDFPKLFRVYSNFRGLKGLKLTGACRTGDR	166	
Db	147	PDPAQAAPLTLTADTFCKLFRVYSNFRGLKGLKLTGACRRGDR	192	

RESULT 6
I46401
erythropoietin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-AUG-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: I46401; I47077
R:Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on p
A:Reference number: I46401; MUID:93351736; PMID:8349021
A:Accession: I46401
A:Status: translated
A:Molecule type: mRNA

A;Residues: 1-194 <FUX>
A;Cross-references: UNIPROT:P33709; EMBL:224681; NID:G395049; PIDN:CAA80848.1; PID:G395050;
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homology
A;Reference number: I46083; MUID:9372347; PMID:8364201
A;Accession: I47077
A;Status: translated from GB/EMBL/DBJ

A;Residues: 4-15,'L',17-107,'P',109-194 <WEN>
A;Cross-references: GB:I0610; NID:g165876; PIDN:AAA31518.1; RID:g165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of
C;Function:
A;Description: the primary inducer of erythrocyte formation
C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-194/Product: erythropoietin #status predicted <MAT>
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,I10/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match	81.1%;	Score	690.5;	DB	1;	Length	194;
Best Local Similarity	82.0%;	Pred. No.	2e-58;				
Matches	137;	Conservative	9;	Mismatches	20;	Indels	1;
						Gaps	1
QY	1	APPRICDSRLVRLYLEAKAENITTGCAEHCSSLNENITVPDTKNFYAKKMEV	QOQA	60			
				:	:	:	:
Db	28	APPRICDSRLVRLYLEAKAENATMGCAEGCSFSENITVPDTKNFYAKKMEV	QOQA	87			
				:	:	:	:
QY	61	VEVWGLALLSEAVLRGQALLVNSQPEWPLQLHVDKAVGLRSLLTLRLALGAAQKEAS	120				
				:	:	:	:
Db	88	LEVWGLALLSEAVFRGQALLANASQCEALRLRHVDKAVGLRSLLTLRLALGAAQKEAIP	147				
				:	:	:	:
QY	121	PPDAA-SAAPRTITADTRFLFRVYSNFLRGKLLYTGACACTGDR	166				
				:	:	:	:
Db	148	LDADTPSAPIRIETVDALSKIEFIYSNEIRGKLLYTGACACTGDR	194				
				:	:	:	:

RESULT 7
A24902 erythropoietin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
A;Accession: A24902; A24901 R;Shoenaker, C.B.; Mitsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A;Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A;Reference number: A24902; PMID:87039105; PMID:3773894
A;Accession: A24902
A;Molecule type: DNA
A;Residues: 1-192 <SHO>
A;Cross-references: UNIPROT:P07321
A;Note: the authors translated the codon TTA for residue 43 as Phe, TTA for residue 43 as Asn.
R;McDonald, J.D., Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A;Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene.
A;Reference number: A24901; PMID:87039104; PMID:3022133

A:Molecule type: DNA
A:Residues: 1-67, 'P', 69-192 <MCD>
A:Cross-references: GB:M12930; NID:G193086; PIDN:AAA37570.1; PID:G387152
C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C:Genetics: 5/1; 52/3; 81/3; 141/3
A:introns: 5/1; 52/3; 81/3; 141/3
C:Function:
A:Description: the primary inducer of erythrocyte formation
C:Superfamily: erythropoietin
C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-192/Product: erythropoietin #status predicted <MAT>
F:33-187,55-165/disulfide bonds: #status predicted
F:50,84,109/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.6%; Score 686; DB 1; Length 192;
Best Local Similarity 79.5%; Pred. No. 5.2e-58;
Matches 132; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 60
DB 27 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 87 IEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 146
QY 121 PPDAASAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 166
DB 147 PPDTPPAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 192

RESULT 8
JC7699
erythropoietin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C:Accession: JC7699
R:Vilalta, A.; Wu, D.; Margalith, M.; Hobart, P.
Biochem. Biophys. Res. Commun. 284, 823-827, 2001
A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
A:Reference number: JC7699; MUID:21290682; PMID:11396976
A:Contents: Kidney
A:Accession: JC7699
A:Molecule type: DNA
A:Residues: 1-195 <VIL>
A:Cross-references: GB:AF290943
C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver cytes.
C:Genetics:
A:Gene: epo
C:Superfamily: erythropoietin
C:Keywords: Glycoprotein; kidney

Query Match 80.6%; Score 685.5; DB 2; Length 195;
Best Local Similarity 81.4%; Pred. No. 5.9e-58;
Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 60
DB 29 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 88
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 89 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 148
QY 121 PPDAASAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 166
DB 149 PPDTPPAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 195

RESULT 9
I46578
erythropoietin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46578
R:Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46578
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <MEN>
A:Cross-references: UNIPROT:P49157; GB:L10607; NID:G164445; PIDN:AAA31029.1; PID:G164446
C:Superfamily: erythropoietin

Query Match 80.3%; Score 683; DB 2; Length 190;
Best Local Similarity 82.1%; Pred. No. 9.9e-58;
Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 60
DB 23 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 82
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 83 MEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 142
QY 121 PPDAASAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 166
DB 143 LPDASPSSAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 190

RESULT 10
I46199
erythropoietin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46199
R:Men, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
A:Reference number: I46083; MUID:93372347; PMID:8364201
A:Accession: I46199
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <MEN>
A:Cross-references: UNIPROT:P33707; GB:L113027; NID:G290087; PIDN:AAA30842.1; PID:G552347
C:Superfamily: erythropoietin

Query Match 75.0%; Score 638; DB 2; Length 175;
Best Local Similarity 81.0%; Pred. No. 1.8e-53;
Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 60
DB 23 APPRLICDSRVLYRYLLEAKEENITTCGAHCSLNENITVPDTKNFYANKRMEVGOQA 82
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 83 LEVWQGLALLSEAVLRGQALLVNSQPWEPLQHVVDKAVSGLSRLTLLRALGAQKEAIS 142
QY 121 PPDAASAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 153
DB 143 LPEASAPLRTITADTFKLFYVSNFLRGKLYTGEACRTGDR 175

RESULT 11
G02729
thrombopoietin - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02729
R:Im, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01637
A:Accession: G02729
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <IMX>
A:Cross-references: EMBL:U59493; NID:G1401245; PIDN:AA03392.1; PID:G1401246
C:Genetics:
A:Gene: htpro

Query Match 10.6%; Score 90; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.74;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

A;Cross-references: GDB:374007; OMIM:600044
A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein

Query Match 10.5%; Score 89; DB 2; Length
Best Local Similarity 26.3%; Pred.No. 0.92; Matches 41; Conservative 20; Mismatches 75; In

QY 1 APRRLCDSRVLEBRYLLEAKENITTCGAECISLNENITVP
DB 24 APP--ACDLRYSKLLRDSHVLHSRLSQCPVEVPLETPVLLP
QY 61 VEVWQGLALISEAVL--RQALLVNSQWPEPLQLHVDKAVS
DB 82 QDILGAVTLLGCVMAARGQLGPTCUSSLLGQLSGQVRLLLGA
QY 119 ISPPDAASAAPLRTITADTFKLFVRYNSFLRGKLG 154
DB 133 -LPPQG-----RTTAHKDPNAIFLSFQHLRGKVR 161

RESULT 13
AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta c
C;Species: Yersinia pestis.
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Steven
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causativ
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:O8ZDC8; GB:AL590842; PIDN:CA
C;Genetics:
C;Accession: AB0959
C;Superfamily: ribonucleoside-diphosphate reductase beta
C;Keywords: oxidoreductase

Query Match 10.3%; Score 88; DB 2; Length
Best Local Similarity 25.2%; Pred.No. 1; Matches 34; Conservative 20; Mismatches 59; In

QY 38 NITVPDTKVFYAKRMVEGQAVVEWQGLLSEAVLRGQAL
DB 2 NVVKETIRISAINWNKIE-DKQLEVN--RLTSNFWLPEKVP
QY 97 ---KAVSGLSRLTLLRLRAGQ---KEAISPPDAASAAPLRTI
DB 59 LTRIVFTGLTLDITQNTLGALPKDAITPHEAIFSNISFM
QY 151 GKLLYTGACRTGD 165
DB 117 -----CLTSD 121

RESULT 14
AB0959
Solute binding receptor protein [imported] - Salmonella en
C;Species: Salmonella enterica subsp. enterica serovar Typh
A;Note: this species has also been called Salmonella typh
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_
C;Accession: AB0959
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; p
S. S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds

Search completed: December 3, 2004, 13:38:45
Job time : 14.0393 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 13:06:58 ; Search time 121.366 Seconds
(without alignments)
786.979 Million cell updates/sec

Title: US-10-780-297-2

Perfect score: 851

Sequence: 1 APPRLICDSVLSRYLLEAK.....NFLRGKLYTGACRTGDR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	851	100.0	193	1	EPO_HUMAN	P01588 homo sapien
2	851	100.0	193	2	AAP22357	Aap22357 homo sapi
3	769.5	90.4	192	1	EPO_MACFA	P07865 macaca fasc
4	764.5	89.8	192	1	EPO_MACVU	Q28513 macaca mula
5	728	85.5	192	2	Q867B1	Q867B1 equus cabal
6	711	83.5	192	2	Q867B1	P33708 felis silve
7	706	83.0	192	1	EPO_FELCA	P29676 rattus norv
8	698	82.0	206	2	Q6PNU5	Q6PNU5 canis fam
9	698	82.0	206	2	Q6PNU5	Aas77874 canis fam
10	697.5	82.0	192	1	EPO_BOVIN	P48617 bos taurus
11	694	81.6	192	1	EPO_MOUSE	P07321 mus musculu
12	690.5	81.1	194	1	EPO_SHEEP	P33709 ovies aries
13	685.5	80.6	195	2	Q9GKA2	Q9GKA2 cryctolagus
14	685.5	80.6	195	2	Q9GKA3	Q9GKA3 cryctolagus
15	683	80.3	190	1	EPO_PIG	P49157 sus scrofa
16	683	80.3	192	2	Q6H8S9	Q6H8S9 spalax gail
17	683	80.3	192	2	Q6H8T0	Q6H8T0 spalax juda
18	683	80.3	192	2	Q6H8T1	Q6H8T1 spalax carm
19	683	80.3	194	2	Q9MYM8	Q9MYM8 sus scrofa
20	679	79.8	192	2	Q6H8T2	Q6H8T2 spalax gola
21	663	77.9	133	2	Q8H288	Q8H288 gorilla gor
22	658	77.3	133	2	Q8H289	Q8H289 pan troglod
23	638	75.0	175	1	EPO_CANFA	P33707 canis fam
24	627	73.7	131	2	Q8H287	Q8H287 pongo pygma
25	607	71.3	133	2	Q8H286	Q8H286 macaca sp.
26	554	65.1	133	2	Q8H285	Q8H285 saquinus oe
27	241	28.3	195	2	Q6UAM1	Q6UAM1 tetraodon n
28	241	28.3	195	2	AAR25698	Aar25698 tetraodon
29	238	28.0	182	2	Q6JV23	Q6JV23 fugu rubri
30	238	28.0	182	2	AAQ72466	AAQ72466 fugu rubr
31	238	28.0	185	2	Q6JV22	Q6JV22 fugu rubrip

32	238	28.0	185	2	AAQ72467	AAQ72467 fugu rubr
33	188	22.1	50	2	Q9QV40	Q9QV40 rattus sp.
34	113	13.3	177	2	Q6IYE9	Q6IYE9 gallus gall
35	109	12.8	352	1	TPO_CANFA	P42705 canis fam
36	89	10.5	353	1	TPO_HUMAN	P40225 homo sapien
37	88	10.3	323	2	Q8ZDC8	Q8ZDC8 homo sapien
38	88	10.3	323	2	AAS62651	Aas62651 yersinia pe
39	87.5	10.3	346	2	Q8ZM5	Q8ZM5 yersinia
40	87.5	10.3	346	2	Q8ZK24	Q8ZK24 salmonella
41	87.5	10.3	432	2	Q7QDZ2	Q7QDZ2 anopheles g
42	85	10.0	339	1	MURB_PSEAE	Q9hzm7 pseudomonas
43	85	10.0	3722	2	P94873	P94873 lysobacter
44	83.5	9.8	296	2	Q8ZAY4	Q8ZAY4 yersinia pe
45	83.5	9.8	296	2	AAS64044	Aas64044 yersinia

ALIGNMENTS

RESULT 1

ID	EPO_HUMAN	STANDARD	PRT	193 AA
AC	P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	Name=EPO;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85137899; PubMed=3838366;			
RA	Jacobs K., Shoemaker C., Ruderstorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.;			
RT	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Suggs S., Lin C.-H., Browne J.K., Smalling R., Egrie J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
RN	[3]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=99018118; PubMed=979793;			
RA	Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 550 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
RN	[4]			
RN	SEQUENCE FROM N.A.			
RP	Rupert J.L., Hochachka P.W.;			
RA	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RN	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RN	SEQUENCE OF 58-193 FROM N.A., AND VARIANTS HEPATOCELLULAR CARCINOMA			
RP	131-AGN-PHE-132 AND GLN-149.			
RX	MEDLINE=93384593; PubMed=8396923;			
RA	Punakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
RN	[6]			

SEQUENCE OF 28-193, AND DISULFIDE BONDS.
 TISSUE=Urine;
 MEDLINE=86140080; PubMed=3949763;
 Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
 "Structural characterization of human erythropoietin.";
 J. Biol. Chem. 261:3116-3121(1986).
 [7]
 PRELIMINARY SEQUENCE OF 28-57.
 MEDLINE=84135751; PubMed=6698989;
 Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
 Goto M.;
 "Isolation of human erythropoietin with monoclonal antibodies.";
 J. Biol. Chem. 259:2707-2710(1984).
 [8]
 STRUCTURE OF CARBOHYDRATES.
 MEDLINE=88153657; PubMed=3346214;
 Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
 Kobata A.;
 "Comparative study of the asparagine-linked sugar chains of human
 erythropoietins purified from urine and the culture medium of
 recombinant Chinese hamster ovary cells.";
 J. Biol. Chem. 263:3657-3663(1988).
 [9]
 STRUCTURE OF CARBOHYDRATES.
 MEDLINE=89118279; PubMed=3219367;
 Sasaki H., Ochi N., Dell A., Fukuda M.;
 "Site-specific glycosylation of human recombinant erythropoietin:
 analysis of glycopeptides or peptides at each glycosylation site by
 fast atom bombardment mass spectrometry.";
 Biochemistry 27:8618-8626(1988).
 [10]
 STRUCTURE OF CARBOHYDRATES.
 MEDLINE=92314463; PubMed=1820196;
 Takeuchi M., Kobata A.;
 "Structures and functional roles of the sugar chains of human
 erythropoietins.";
 Glycobiology 1:337-346(1991).
 [11]
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
 Syed R.S., Reid S.W., Li C., Cheatham J.C., Roki K.H., Liu B.,
 Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
 Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
 Egnie J., Stroud R.M.;
 "Efficiency of signalling through cytokine receptors depends
 critically on receptor orientation.";
 Nature 395:511-516(1998).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 regulation of erythrocyte differentiation and the maintenance of a
 physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 and by liver of fetal or neonatal mammals.
 CC -!- PHARMACEUTICAL: Used for the treatment of anemia. Available under
 the names Epogen (Amgen), Epogen (Chugai), Epomax (Eli Lilly), Eprex
 (Janssen-Cilag), NeoRecormon or Recormon (Roche), and Procrit
 (Ortho Biotech). Variations in the glycosylation pattern of EPO
 distinguishes these products. Epogen, Epogen, Eprex and Recormon
 are generically known as epoetin alfa, NeoRecormon and Recormon as
 epoetin beta and Epomax as epoetin omega.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC -!- DATABASE: NCBIR&D Systems' cytokine source book: EPO;
 WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=197".

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; X02158; CAA26095.1; -

DR EMBL; X02157; CAA26094.1; -
 DR EMBL; M11319; AAS2400.1; -
 DR EMBL; AF053356; AAC78791.1; -
 DR EMBL; AF202308; AAF23132.1; -
 DR EMBL; AF202306; AAF23132.1; JOINED.
 DR EMBL; AF202307; AAF23132.1; JOINED.
 DR EMBL; AF202310; AAF23133.1; -
 DR EMBL; AF202309; AAF23133.1; JOINED.
 DR EMBL; AF202311; AAF17572.1; -
 DR EMBL; AF202314; AAF23134.1; -
 DR EMBL; AF202312; AAF23134.1; JOINED.
 DR EMBL; AF202313; AAF23134.1; JOINED.
 DR EMBL; S65458; RAD13964.1; -
 DR PIR; A01855; ZUHU
 DR PDB; 1BUJ; NMR; A=28-193.
 DR PDB; 1CN4; X-ray; C=28-193.
 DR PDB; 1BER; X-ray; A=28-193.
 DR GlycoSuiteDB; P01588; -
 DR Genew; HGNC:3415; EPO.
 DR MIM; 133170; -
 GO; GO:0005615; C:extracellular space; TAS.
 GO; GO:0006950; P:response to stress; TAS.
 GO; GO:0006950; P:response to stress; TAS.
 DR InterPro; IPR009075; 4-helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythropoietin.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PIRSF; PIRSF001951; EPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR 3D-structure; Direct protein sequencing; Erythrocyte maturation;
 KW Glycoprotein; Hormone; Pharmacological; Polymorphism; Signal.
 FT SIGNAL 1 27 Erythropoietin.
 FT CHAIN 28 193 Removed in mature form (Probable).
 FT PROPEP 190 193
 FT DISULFID 34 188
 FT DISULFID 56 60
 FT CARBOHYD 51 51 N-linked (GlcNAc...).
 FT CARBOHYD 65 65 /FTid=CAR_000052.
 FT CARBOHYD 110 110 N-linked (GlcNAc...).
 FT CARBOHYD 153 153 N-linked (GlcNAc...).
 FT CARBOHYD 131 132 O-linked (GalNAc...).
 FT VARIANT SL -> NF (in an hepatocellular carcinoma).
 FT VARIANT 149 /FTid=VAR_009870.
 FT VARIANT 40 40 P -> Q (in an hepatocellular carcinoma).
 FT CONFLICT 85 85 E -> Q (in Ref. 1; CAA26095).
 FT CONFLICT 140 140 Q -> QO (in Ref. 5).
 FT CONFLICT 32 34 G -> R (in Ref. 1; CAA26095).
 FT HELIX 36 52
 FT HELIX 36 52
 FT HELIX 53 55
 FT TURN 57 58
 FT STRAND 61 68
 FT STRAND 73 73
 FT HELIX 75 78
 FT TURN 79 80
 FT HELIX 83 109
 FT HELIX 118 138
 FT TURN 139 140
 FT HELIX 141 147
 FT TURN 148 149
 FT STRAND 160 164
 FT HELIX 165 177
 FT TURN 178 178
 FT HELIX 179 188
 SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
 Query Match 100.0%; Score 851; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 6.6e-72; Indels 0; Gaps 0;
 Matches 166; Conservative 0; Mismatches 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 193

RESULT 2

AAAP22357 PRELIMINARY; PRT; 193 AA.
AC AAP22357;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein EPO.
GN EPO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Wilson R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T., Sun H.;
RT "The sequence of Homo sapiens BAC clone RP11-336D7.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009488; AAP22357.1; .
KW Hypothetical protein.
SQ SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;

Query Match 100.0%; Score 851; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-72;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 193

RESULT 3

EPO_MACFA

ID AC P07855; STANDARD; PRT; 192 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87055236; PubMed=2877922;
RA Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,
RA Fox G.M., Chen K.K., Castro M., Suggs S.;
RT "Monkey erythropoietin gene: Cloning, expression and comparison with
RT the human erythropoietin gene.";
RL Gene 44:201-209(1986).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M18189; AAA36841.1; .
DR PIR; JQ0173; JQ0173.
DR HSP; P01588; ICN4.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001323; EPO TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PRO0272; ERYTHROPTN.
DR PROSITE; PS00817; EPO TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 27
FT CHAIN 28 192
FT Disulfid 34 187
FT Disulfid 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CARBOHYD 152 152
SQ SEQUENCE 192 AA; 21113 MW; E8A900F442AD4522 CRC64;
Query Match 90.4%; Score 769.5; DB 1; Length 192;
Best Local Similarity 91.6%; Pred. No. 3.1e-64;
Matches 152; Conservative 7; Mismatches 6; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 60
DB 28 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLVDKAVSGLSLTLLRALGAKQEAIS 146
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 166
DB 147 PPDAASAAPLRTITADTFKRLFRVYSNFRGLKLYTGEACRTGDR 192

```

RESULT 4
EPO_MACMU STANDARD; PRT; 192 AA.
AC Q28513;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RA "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -1- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -1- SIMILARITY: Belongs to the EPO / TPO family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L10609; AAA36842.1; -.
CC PIR; I84613; I84613.
CC HSP; P01588; 1CN4.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT CHAIN 1 27
FT SIGNAL 1 27
FT CHAIN 28 192
FT DISULFID 34 187
FT DISULFID 56 60
FT CARBOHYD 51 51
FT CARBOHYD 65 65
FT CARBOHYD 110 110
FT CARBOHYD 152 152
FT CARBOHYD 152 152
FT SEQUENCE 192 AA; 21081 MW; 275560A264628CD1 CRC64;

Query Match 89.8%; Score 764.5; DB 1; Length 192;
Best Local Similarity 90.4%; Pred. No. 9.2e-64;
Matches 150; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 APRILCDSRVLYRLLLEAKEAENITTCGAHCSLSNENITVPDTKNFYAKKMEVGGQA 60
DB 28 APRILCDSRVLYRLLLEAKEAENITTCGSLSNENITVPDTKNFYAKKMEVGGQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWFPLQLHVDKAVSGLSLTLLRALGAKQEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWFPLQLHMDKAVSGLSLTLLRALGAKQEAIS 146

RESULT 5
Q967B1 PRELIMINARY; PRT; 192 AA.
AC Q867B1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythropoietin.
GN Name=EPO;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA PubMed=14719696;
RA Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
RA Kijima-Suda I.;
RA "Nucleotide sequence of equine erythropoietin and characterization of
RT region-specific antibodies.";
RL Am. J. Vet. Res. 65:15-19(2004).
DR EMBL; AB100030; BAC55239.1; -.
DR HSP; P01588; 1BUU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005128; F:erythropoietin receptor binding; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005179; 4 helix cytokine.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PIRSF; PIRSF001951; EPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
DR SEQUENCE 192 AA; 20984 MW; E02D09849B09C4F CRC64;

Query Match 85.5%; Score 728; DB 2; Length 192;
Best Local Similarity 84.9%; Pred. No. 2.5e-60;
Matches 141; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 APRILCDSRVLYRLLLEAKEAENITTCGAHCSLSNENITVPDTKNFYAKKMEVGGQA 60
DB 27 APRILCDSRVLYRLLLEAKEAENITTCGAHCSLSNENITVPDTKNFYAKKMEVGGQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWFPLQLHVDKAVSGLSLTLLRALGAKQEAIS 120
DB 87 VEVWQGLALLSEAVLRGQALLVNSQPWFPLQLHVDKAVSGLSLTLLRALGAKQEAIS 146

RESULT 6
EPO_FELCA STANDARD; PRT; 192 AA.
AC P33708;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Erythropoietin precursor.
GN Name=EPO;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RN Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RP [2]
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993)
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U06685; AAA18282.1; -;
CC EMBL; L10606; AAA30807.1; -;
CC PIR; I46083; I46083.
CC HSSP; P01588; 1BUY.
CC
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
CC SIGNAL 1 26
CC CHAIN 27 192
CC DISULFID 33 187
CC FT By similarity.
CC FT By similarity.
CC FT By similarity.
CC FT N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 50 50
CC FT CARBOHYD 64 64
CC FT CARBOHYD 109 109
CC FT N-linked (GlcNAc...) (Potential).
CC FT CONFLICT 44 44 G->E (in Ref. 2).
CC SEQUENCE 192 AA; 20914 MW; 61C5EAF5E937293 CRC64;

CC Query Match 83.5%; Score 711; DS 1; Length 192;
CC Best Local Similarity 83.7%; Pred. No. 1e-58;
CC Matches 139; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

CC 1 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 60
CC 27 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 86
CC 61 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 120
CC 87 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 146

CC Query Match 83.0%; Score 706; DB 1; Length 192;
CC Best Local Similarity 82.5%; Pred. No. 2.9e-58;
CC Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

CC 1 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 60
CC 27 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 86
CC 61 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 120
CC 87 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 146
CC 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGTGACRTGDR 166
CC 147 LPEATSAAPLRTITADTFKLFVYNSFLRGKLYTGTGACRTGDR 192

CC RESULT 7
CC EPO_RAT
CC ID EPO_RAT STANDARD; PRT; 192 AA.
CC AC P29676; P70504;
CC DT 01-APR-1993 (Rel. 25, Created)
CC DT 01-APR-1993 (Rel. 25, Last sequence update)
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Erythropoietin precursor.
GN Name:Epo;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=93042015; PubMed=1420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Sasaki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
CC [2]
CC SEQUENCE OF 4-192 FROM N.A.
CC STRAIN=Sprague-Dawley; TISSUE=Kidney;
CC MEDLINE=93372347; PubMed=8364201;
CC Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
CC Goodman M., Bunn H.F.;
CC "Erythropoietin structure-function relationships: high degree of
CC sequence homology among mammals.";
CC Blood 82:1507-1516(1993).
CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
CC regulation of erythrocyte differentiation and the maintenance of a
CC physiological level of circulating erythrocyte mass.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
CC and by liver of fetal or neonatal mammals.
CC -!- SIMILARITY: Belongs to the EPO / TPO family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D10763; BAA01593.1; -;
CC EMBL; L10608; AAA41126.1; -;
CC PIR; S28148; S28148.
CC HSSP; P01588; 1CN4.
CC
CC RGD; 2559; EPO.
CC InterPro; IPR009079; 4 helix_cytokine.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PIRSF; PIRSF001951; EPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
CC SIGNAL 1 26
CC CHAIN 27 192
CC DISULFID 33 187
CC FT By similarity.
CC FT By similarity.
CC FT By similarity.
CC FT N-linked (GlcNAc...) (By similarity).
CC FT CARBOHYD 50 50
CC FT CARBOHYD 64 64
CC FT CARBOHYD 109 109
CC FT N-linked (GlcNAc...) (By similarity).
CC SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;

CC Query Match 83.0%; Score 706; DB 1; Length 192;
CC Best Local Similarity 82.5%; Pred. No. 2.9e-58;
CC Matches 137; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

CC 1 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 60
CC 27 APRRLICDSRVLYRYLLLEAKEAENITTCGAHCSLNENITVPTKYNFYAKRMEVGGQA 86
CC 61 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 120
CC 87 VEVWQGLALLSEALVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTLTLLRALCAQKEAIS 146
CC 121 PPDAASAAPLRTITADTFKLFVYNSFLRGKLYTGTGACRTGDR 166

Matches 139; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYLEAEAEENITTCAGHCSLNENITVPDTKNFYAKRMEVQQA 60
 Db 26 APPRLICDSRVLYLEAEAEENITTCAGHCSLNENITVPDTKNFYAKRMEVQQA 85
 QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Db 86 LEVWQGLALLSEAILRQALLANASQPCEARLHVDKAVSGLSRLTLLRALGAQKEAIS 145
 QY 121 PPDAASAAPIRTITADTFKLFVYVSNFLRGKLYTGACRTGDR 166
 Db 146 LPDATSAAPLRAFTVDALSKLFRIVSNFLRGKLYTGACRTGDR 192

RESULT 11
 EPO_MOUSE
 ID EPO_MOUSE STANDARD; PRT; 192 AA.
 AC P07321;
 DT 01-APR-1998 (Rel. 07, Created)
 DT 01-APR-1998 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=Epo;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoenaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RL Mol. Cell. Biol. 6:849-858(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RL Mol. Cell. Biol. 6:842-848(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Teui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RC STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia I332 cells results from a rearrangement between the G-
 RT protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999(1997).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; M12482; AAA37568.1; -;
 CC EMBL; M12930; AAA37570.1; -;
 CC EMBL; AF312033; AAK38825.1; -;
 CC EMBL; Y11971; CAA72707.1; -;
 CC PIR; A24902; A24902.
 CC HSSP; P01588; 1CN4.
 CC MGD; MGI:95407; EPO.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR001323; EPO_TPO.
 CC InterPro; IPR003013; Erythroptn.
 CC Pfam; PF00758; EPO_TPO; 1.
 CC PIRSF; PIRSF001951; EPO; 1.
 CC PRINTS; PR00272; ERYTHROPTN.
 CC PROSITE; PS00817; EPO_TPO; 1.
 CC Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 192 Erythropoietin.
 FT DISULFID 33 187 By similarity.
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc...) (By similarity).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;
 Query Match 81.6%; Score 694; DB 1; Length 192;
 Best Local Similarity 80.1%; Pred. No. 4e-57;
 Matches 133; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
 QY 1 APPRLICDSRVLYLEAEAEENITTCAGHCSLNENITVPDTKNFYAKRMEVQQA 60
 Db 27 APPRLICDSRVLYLEAEAEENITTCAGHCSLNENITVPDTKNFYAKRMEVQQA 86
 QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 Db 87 LEVWQGLALLSEAILRQALLANASQPCPETIQLHIDKAVSGLSRLTLLRALGAQKEAIS 146
 QY 121 PPDAASAAPIRTITADTFKLFVYVSNFLRGKLYTGACRTGDR 166
 Db 147 PPDTPPAPLRLTVDFCKLFRVYANFLRGKLYTGACRTGDR 192

RESULT 12
 EPO_SHEEP
 ID EPO_SHEEP STANDARD; PRT; 194 AA.
 AC P33709; O28572;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor.
 GN Name=EPO;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93351736; PubMed=8349021;
 RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
 RT "The sheep erythropoietin gene: molecular cloning and effect of
 RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
 RT adult sheep.";
 RL Mol. Cell. Endocrinol. 93:107-116(1993).
 RN [2]
 RP SEQUENCE OF 4-194 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

Czelusniak J., Goodman M., Bunn H.F.;
"Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
Blood 82:1507-1516(1993).
-!- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
or send an email to license@isb-sib.ch).

EMBL; Z24681; CAA80848.1; --
EMBL; L10610; AAA31518.1; --
PIR; I46401; I46401.
HSSP; P01588; 1CN4.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001323; EPO_TPO.
InterPro; IPR003013; Erythroptn.
Pfam; PF00758; EPO_TPO; 1.
PIRSF; PIRSF001951; EPO; 1.
PRINTS; PRO0272; ERYTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
SIGNAL 1 27 By similarity.
CHAIN 28 194 Erythropoietin.
DISULFID 34 189 By similarity.
DISULFID 56 60 By similarity.
FT CARBOHYD 51 51 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT CONFLICT 16 16 F -> L (in Ref. 2).
FT CONFLICT 108 108 L -> P (in Ref. 2).
SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;
Query Match 81.1%; Score 690.5; DB 1; Length 194;
Best Local Similarity 82.0%; Pred.No. 8.6e-57;
Matches 137; Conservative 9; Mismatches 20; Indels 1; Gaps 1;
QY 1 APPRLICDSRVLYRLYLEAEAEENITTCGAHCSSLNENITVPDTKNFYAWKNEVCGQA 60
DB 28 APPRLICDSRVLYRLYLEAEAEENATGCAEGCSFENITVPDTKNFYAWKNEVCGQA 87
QY 61 VEVWQGLALISEAVLRQALLVNSQPSWPEQLQHVDDKAVSGLRSLTLLRALGAKQAEIS 120
DB 88 LEVWQGLALISEAIFRQALLANASQCEALRLHVDKAVSGLRSLTLLRALGAKQAEIP 147
QY 121 PPDAASAAPLRTTATFKLFRVYSNFKRLKLYTGCAERTGDR 166
DB 148 LPDTPSAAPLRIFETVDALSKLFRIYSNFKRLKLYTGCAERCGRDR 194
RESULT 13
Q9GKA2 PRELIMINARY; PRT; 195 AA.
ID Q9GKA2
AC Q9GKA2
DT 01-NAR-2001 (TREMBLrel. 16, Created)
DT 01-NAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-NAR-2004 (TREMBLrel. 26, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RX [1]

Matches 136; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAKRMEVQQA 60
 Db 29 APARLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAKRMEVQQA 88
 QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 Db 89 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 148
 QY 121 PPDA--AAAPLRTITADTFKLPVYNSFLRGKLYTGEACRTGDR 166
 Db 149 PPEAASAAPLRTVAADTLCKLFRVYNSFLRGKLYTGEACRTGDR 195

RESULT 15

EPO_PIG STANDARD; PRT; 190 AA.
 AC P49157;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Erythropoietin precursor (Fragment).
 GN Name=EPO;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: Erythropoietin is the principal hormone involved in the
 CC regulation of erythrocyte differentiation and the maintenance of a
 CC physiological level of circulating erythrocyte mass.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
 CC and by liver of fetal or neonatal mammals.
 CC -!- SIMILARITY: Belongs to the EPO / TPO family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L10607; AAA31029.1; -;
 DR PIR; I46578; I46578.
 DR HSSP; P01588; 1CN4.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 DR Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 KW NON_TER 1 1
 FT SIGNAL <1 22 Potential.
 FT CHAIN 23 190 Erythropoietin.
 FT DISULFID 29 185 By similarity.
 FT DISULFID 51 55 By similarity.
 FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;

Query Match 80.3%; Score 683; DB 1; Length 190;
 Best Local Similarity 82.1%; Pred. No. 4.3e-56;
 Matches 138; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
 QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAKRMEVQQA 60
 Db 23 APARLICDSRVLYRLLEAKEAENITTCGAHCHSLNENITVPDTKKNFYAKRMEVQQA 82
 QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 Db 83 MEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIP 142
 QY 121 PPDA--AAAPLRTITADTFKLPVYNSFLRGKLYTGEACRTGDR 166
 Db 143 LPDASPSATPLRTFAVDTLCKLFRVYNSFLRGKLYTGEACRTGDR 190

Search completed: December 3, 2004, 13:38:13
 Job time : 122.366 secs

Page Blank (uspto)